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SEQUENCE LISTING

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<120> SYNTHETIC GENES FOR ENHANCED EXPRESSION

<130> B583:40608

<140> US 09/734,237

<141> 2000-12-08

<150> 09/494,921

<151> 2000-01-31

<160> 79

<170> PatentIn version 3.1

<210> 1

<211> 1197

<212> DNA

<213> Pseudomonas putida

<400> 1

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cccaccgtgg aatacggcg tgctgtcttt gccggcgagc aggccgggca tttctacagc	180
cgcattctcca accccaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc	240
gaggccgggc tggcgctggc ctcgggcatg ggggcgatca cgtccacgct atggacactg	300
ctgcgccccg gtgacgaggt gctgctgggc aacaccctgt acggctgcac ctttgcttc	360
ctgcaccacg gcatcggcga gttcggggtc aagctgcgcc atgtggacat ggccgacctg	420
caggcactgg aggcggccat gacgccggcc acccggtga tctatttcga gtcgccggcc	480
aacccaaca tgcacatggc cgatatcgcc ggctggcgca agattgcacg caagcacggc	540
gcgaccgtgg tggctgacaa cacctactgc acgccgtacc tgcaacggcc actggagctg	600
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gacatgaccg gtgcggtgct ctgcgcccat gacgccgcac tgttgatgcy cggcatcaag	780
accctcaacc tgcgcatgga ccggcactgc gccaacgctc aggtgctggc cgagttcctc	840
gcccggcagc cgcaggtgga gctgatccat taccggggcc tggcgagctt cccgcagtac	900
accctggccc gccagcagat gagccagccg ggccggcatga tcgccttcga actcaagggc	960

ggcatcgggtg ccgggcgggcg gttcatgaac gccctgcaac tggtcagccg cgcggtgagc 1020
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 ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcggttgtc ggtggggctg 1140
 gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgctga 1197

<210> 2
 <211> 399
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Pseudomonas putida methionine gamma-lyase amino acid sequence, with a non-naturally occurring glycine residue inserted at position 2

<400> 2

Met Gly His Gly Ser Asn Lys Leu Pro Gly Phe Ala Thr Arg Ala Ile
 1 5 10 15

His His Gly Tyr Asp Pro Gln Asp His Gly Gly Ala Leu Val Pro Pro
 20 25 30

Val Tyr Gln Thr Ala Thr Phe Thr Phe Pro Thr Val Glu Tyr Gly Ala
 35 40 45

Ala Cys Phe Ala Gly Glu Gln Ala Gly His Pro Tyr Ser Arg Ile Ser
 50 55 60

Asn Pro Thr Leu Asn Leu Leu Gln Ala Arg Met Ala Ser Leu Glu Gly
 65 70 75 80

Gly Glu Ala Gly Leu Ala Leu Ala Ser Gly Met Gly Ala Ile Thr Ser
 85 90 95

Thr Leu Tyr Thr Leu Leu Arg Pro Gly Asp Glu Val Leu Leu Gly Asn
 100 105 110

Thr Leu Tyr Gly Cys Thr Phe Ala Phe Leu His His Gly Ile Gly Glu
 115 120 125

Phe Gly Val Lys Leu Arg His Val Asp Met Ala Asp Leu Gln Ala Leu
 130 135 140

Glu Ala Ala Met Thr Pro Ala Thr Arg Val Ile Tyr Phe Glu Ser Pro
145 150 155 160

Ala Asn Pro Asn Met His Met Ala Asp Ile Ala Gly Val Ala Lys Ile
165 170 175

Ala Arg Lys His Gly Ala Thr Val Val Val Asp Asn Thr Tyr Cys Thr
180 185 190

Pro Tyr Leu Gln Arg Pro Leu Gln Leu Gly Ala Asp Leu Val Val His
195 200 205

Ser Ala Thr Lys Tyr Leu Ser Gly His Gly Asp Ile Thr Ala Gly Ile
210 215 220

Val Val Gly Ser Gln Ala Leu Val Asp Arg Ile Arg Leu Gln Gly Leu
225 230 235 240

Lys Asp Met Thr Gly Ala Val Leu Ser Pro His Asp Ala Ala Leu Leu
245 250 255

Met Arg Gly Ile Lys Thr Leu Asn Leu Arg Met Asp Arg His Cys Ala
260 265 270

Asn Ala Gln Val Leu Ala Glu Phe Leu Ala Arg Gln Pro Gln Val Glu
275 280 285

Leu Ile His Tyr Pro Gly Leu Ala Ser Phe Pro Gln Tyr Thr Leu Ala
290 295 300

Arg Gln Gln Met Ser Gln Pro Gly Gly Met Ile Ala Phe Glu Leu Lys
305 310 315 320

Gly Gly Ile Gly Ala Gly Arg Arg Phe Met Asn Ala Leu Gln Leu Phe
325 330 335

Ser Arg Ala Val Ser Leu Gly Asp Ala Glu Ser Leu Ala Gln His Pro
340 345 350

Ala Ser Met Thr His Ser Ser Tyr Thr Pro Glu Glu Arg Ala His Tyr
355 360 365

Gly Ile Ser Glu Gly Leu Val Arg Leu Ser Val Gly Leu Glu Asp Ile
 370 375 380

Asp Asp Leu Leu Ala Asp Val Gln Gln Ala Leu Lys Ala Ser Ala
 385 390 395

<210> 3
 <211> 1202
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Pseudomonas putida methionine gamma-lyase sequence, with glycine codon inserted to incorporate restriction site and numerous naturally occurring codons changed to codons more commonly used in enteric bacteria

<400> 3
 catgggtcac ggctccaaca aactgccggg ctttgctacc cgcgctatcc accacgggta 60
 tgaccgcgag gatcacggtg gtgcactggt tccgccggtt taccagactg ctactttcac 120
 cttcccgacc gttgaatacg gcgctgcgtg ctttgctggc gaacaggctg gtcacttcta 180
 ctcccgatc tccaaccga cctgaacct gctggaagca cgtatggcat ctctggaagg 240
 cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta cctgtggac 300
 cctgctgcgt cggggtgacg aagttctgct gggcaacacc ctgtatgggt gtacttttgc 360
 tttcctgcac cacggtatcg gtgaattcgg cgtaaactg cgtcacgtag atatggctga 420
 cctgcaggca ctggaagcgg ctatgacccc ggctaccggt gttatctact tcgaatcccc 480
 ggctaaccgc aacatgcaca tggctgacat cgcagggtgt gctaaaatcg ctcgtaagca 540
 cggcgctacc gtagttgttg ataacaccta ctgtactccg tacctgcaac gtccgctgga 600
 actgggcgct gacctgggtt ttactccgc tactaaatac ctgtccggcc acggcgacat 660
 cactgctggc atcgtagtag gctcccaggc actgggtgac cgtatccgtc tgcaagggtc 720
 gaaagacatg accggcgctg ttctgtcccc gcacgacgca gcactgctga tgcgtggtat 780
 caagaccctg aacctgcgta tggaccgtca ctgtgctaac gctcaggtag tggctgaatt 840
 cctggctcgt cagccgcagg tagaactgat ccactatccg ggctgggtt cttcccgca 900
 gtacactctg gcacgtcagc agatgtccca gccgggcggt atgatcgctt tcgaactgaa 960
 ggggtggcatc ggcgctggtc gtcgtttcat gaacgctctg cagctgttct cccgtgcggt 1020
 ttccctgggt gacgctgaat cctggcgca gcaccggca tccatgactc actcctcta 1080
 cactccggaa gaacgtgcgc actacggcat ctccgaaggc ctggttcgtc tgtctggttg 1140

tctggaagac atcgatgata tgctggcaga cgttcagcag gctctgaagg ctagcgcttg	1200
ag	1202

<210> 4
 <211> 426
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Cloning fragment of SEQ ID NO. 3

<400> 4	
catgggtcac ggctccaaca aactgccggg ctttgctacc cgcgctatcc accacggtta	60
tgaccgcag gatcacggtg gtgcaactgg tccgccggtt taccagactg ctactttcac	120
cttcccgacc gttgaatacg gcgctgcgtg ctttgctggc gaacaggctg gtcacttcta	180
ctcccgatc tccaaccga cctgaacct gctggaagca cgtatggcat ctctggaagg	240
cggcgaagct ggtctggcgc tggcatctgg tatgggcgcg atcacctcta ccctgtggac	300
cctgctgcgt ccgggtgacg aagttctgct gggcaacacc ctgtatgggt gtacttttgc	360
tttctgcac cacggtatcg gtgaattcgg cgtaaactg cgtcacgtag atatggctga	420
cctgca	426

<210> 5
 <211> 441
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Cloning fragment of SEQ ID NO. 3

<400> 5	
caagaggcca tgggtcacgg ctccaacaaa ctgccgggct ttgctaccgc cgctatccac	60
cacggttatg accgcagga tcacggtggt gcaactgggtc cgccggttta ccagactgct	120
actttcacct tcccgaccgt tgaatacggc gctgcgtgct ttgctggcga acaggctggt	180
caattctact cccgtatctc caaccgcacc ctgaacctgc tggaagcacg tatggcatct	240
ctggaaggcg gcgaagctgg tctggcgtg gcatctggta tgggcgcgat cacctctacc	300
ctgtggaccc tgctgcgtcc gggtgacgaa gttctgctgg gcaacacct gtatggttgt	360
acttttgctt tctgcacca cggtatcggg gaattcggcg ttaaactgcg tcacgtagat	420
atggctgacc tgcaggcact g	441

<210> 6
<211> 410
<212> DNA
<213> Artificial sequence

<220>
<223> Cloning fragment of SEQ ID NO. 3

<400> 6
ggcactggaa gcggttatga ccccggtac ccgtgttata tacttcgaat ccccggttaa 60
cccgaacatg cacatggctg acatcgcagg tgttgctaaa atcgtcgtgta agcacggcgc 120
taccgtagtt gttgataaca cctactgtac tccgtacctg caacgtccgc tggaactggg 180
cgctgacctg gttgttcact ccgtactaa atacctgtcc ggccacggcg acatcactgc 240
tggcatcgta gtaggctccc aggcaactgt tgaccgtatc cgtctgcaag gtctgaaaga 300
catgaccggc gctgttctgt ccccgcacga cgcagcactg ctgatgcgtg gtatcaagac 360
cctgaacctg cgtatggacc gtcactgtgc taacgctcag gtactggctg 410

<210> 7
<211> 430
<212> DNA
<213> Artificial sequence

<220>
<223> Cloning fragment of SEQ ID NO. 3

<400> 7
gctgacctgc aggcactgga agcggtatg accccggcta cccgtgttat ctacttcgaa 60
tccccggcta acccgaacat gcacatggct gacatcgcag gtgttgctaa aatcgtcgt 120
aagcacggcg ctaccgtagt tgttgataac acctactgta ctccgtacct gcaacgtccg 180
ctggaactgg gcgctgacct ggttgttcac tccgtacta aatacctgtc cggccacggc 240
gacatcactg ctggcatcgt agtaggctcc caggcaactg ttgaccgtat ccgtctgcaa 300
ggctctgaaag acatgaccgg cgctgttctg tccccgcacg acgcagcact gctgatgcgt 360
ggatatcaaga cctgaacct gcgtatggac cgctactgtg ctaacgctca ggtactggct 420
gaattcctgg 430

<210> 8
<211> 366
<212> DNA
<213> Artificial sequence

<220>

<223> Cloning fragment of SEQ ID NO. 3

<400> 8

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aattcctggc tcgtcagccg caggtagaac tgatccacta tccgggcctg gcttccttcc 60
cgcagtacac tctggcacgt cagcagatgt cccagccggg cggtatgata gctttcgaac 120
tgaaggggtg catcggcgct ggtcgtcgtt tcatgaacgc tctgcagctg ttctcccgtg 180
cggtttccct ggggtgacgt gaatccctgg cgcagcaccg ggcattcatg actcactcct 240
cctacactcc ggaagaacgt gcgcactacg gcattctcga aggcctgggt cgtctgtctg 300
ttgggtctga agacatcgat gatctgctgg cagacgttca gcaggctctg aaggctagcg 360
cttgag 366
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<210> 9

<211> 383

<212> DNA

<213> Artificial sequence

<220>

<223> Cloning fragment of SEQ ID NO. 3

<400> 9

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ttccttcccg cagtacactc tggcacgtca gcagatgtcc cagccggggc gtatgatcgc 120
tttcgaactg aaggggtggc tcggcgctgg tcgtcgtttc atgaacgctc tgcagctggt 180
ctcccgtgcg gtttccctgg gtgacgctga atccctggcg cagcaccgcg catccatgac 240
tcaactcctc tacactccgg aagaacgtgc gcactacggc atctccgaag gcctgggttcg 300
tctgtctggt ggtctggaag acatcgatga tctgtggcga gacgttcagc aggctctgaa 360
ggctagcgct tgaggatcca cca 383
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<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/template derived from SEQ ID NO. 3

<400> 10

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caagaggcca tgggtcacgg ctccaacaaa ctg 33
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<210> 11

<211> 114

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/template derived from SEQ ID NO. 3

<400> 11

cacggctcca acaaactgcc gggctttgct accgcgcta tccaccacgg ttatgacctg 60

caggatcacg gtggtgcact ggttcgcgcg gtttaccaga ctgctacttt cacc 114

<210> 12

<211> 116

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/template derived from SEQ ID NO. 3

<400> 12

gcttcagca ggttcagggt cgggttgag atacgggagt agaagtgacc agcctgttcg 60

ccagcaaagc acgcagcgcc gtattcaacg gtcgggaagg tgaaagtagc agtctg 116

<210> 13

<211> 117

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/template derived from SEQ ID NO. 3

<400> 13

ctgaacctgc tggaagcacg tatggcatct ctggaaggcg gcgaagctgg tctggcgctg 60

gcatctggta tgggcgcgat cacctctacc ctgtggacct tgctgcgtcc gggtgac 117

<210> 14

<211> 116

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer/template derived from SEQ ID NO. 3

<400> 14

gccatatcta cgtgacgcag tttaacgccg aattcaccga taccgtggtg caggaaagca 60

aaagtacaac catacagggt gttgccacgc agaacttcgt caccgggacg cagcag 116

<210> 15

<211> 33

<212> DNA

<213> Artificial Sequence

<220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 15
 cagtcgctgc aggtcagcca tatctacgtg acg 33

 <210> 16
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 16
 gctgacctgc aggcactgga agcggctatg acc 33

 <210> 17
 <211> 114
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 17
 ctggaggctg ctatgacccc ggctaccgt gttatctact tcgaatcccc ggctaaccgg 60
 aacatgcaca tggctgacat cgcaggtggt gctaaaatcg ctcgtaagca cggc 114

 <210> 18
 <211> 115
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 18
 ggtatttagt agcggagtga acaaccaggt cagcgcccag ttccagcgga cgttgcaggt 60
 acggagtaca gtaggtgtta tcaacaacta cggtagcgcc gtgcttacga gcgat 115

 <210> 19
 <211> 111
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 19

cactccgcta ctaaatacct gtccggccac ggcgacatca ctgctggcat cgtagtaggc 60
tcccaggcac tggttgaccg tatccgtctg caaggtctga aagacatgac c 111

<210> 20
<211> 115
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer/template derived from SEQ ID NO. 3

<400> 20
gtacctgagc gttagcacag tgacgggtcca tacgcagggt cagggctctg ataccacgca 60
tcagcagtgc tgcgtcgtgc ggggacagaa cagcgccggt catgtctttc agacc 115

<210> 21
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer/template derived from SEQ ID NO. 3

<400> 21
ccaggaattc agccagtacc tgagcgtag cac 33

<210> 22
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer/template derived from SEQ ID NO. 3

<400> 22
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<210> 23
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer/template derived from SEQ ID NO. 3

<400> 23
ctggctcgtc agccgcagggt agaactgatc cactatccgg gcctggcttc cttcccgcag 60
tacactctgg cacgtcagca gatgtcccag ccgggcggta tgate 105

<210> 24
 <211> 106
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 24
 cgtcacccag ggaaaccgca cgggagaaca gctgcagagc gttcatgaaa cgacgaccag 60
 cgccgatgcc acccttcagt tcgaaagcga tcatgccacc cggctg 106

 <210> 25
 <211> 106
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 25
 gcggtttccc tgggtgacgc tgaatccctg gcgcagcacc cggcatccat gactcactcc 60
 tcctacactc cggaagaacg tgcgcactac ggcattctcg aaggcc 106

 <210> 26
 <211> 98
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 26
 caagcgctag ccttcagagc ctgctgaacg tctgccagca gatcatcgat gtcttccaga 60
 ccaacagaca gacgaaccag gccttcggag atgccgta 98

 <210> 27
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer/template derived from SEQ ID NO. 3

 <400> 27
 tgggtgatcc tcaagcgcta gccttcagag cc 32

 <210> 28
 <211> 1197
 <212> DNA

<213> Artificial Sequence

<220>

<223> Methionine gamma-lyase gene derived from *Pseudomonas putida*, having all arginine codons replaced with arginine codons found most commonly in *E. coli*

<400> 28

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cccaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggccgggca tttctacagc      180
cgcatctcca accccaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc      240
gaggccgggc tggcgctggc ctcgggcatg ggggcgatca cgtccacgct atggacactg      300
ctgcgccccg gtgacgaggt gctgctgggc aacaccctgt acggctgcac ctttgccctc      360
ctgcaccacg gcatcggcga gttcggggtc aagctgcgcc atgtggacat ggccgacctg      420
caggcactgg aggcggccat gacgccggcc acccgtgtga tctatttcga gtcgccggcc      480
aaccccaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc      540
gcgaccgtgg tggctgacaa cacctactgc acgccgtacc tgcaacgtcc actggagctg      600
ggcgccgacc tgggtggtgca ttcggccacc aagtaacctga gcggccatgg cgacatcact      660
gctggcattg tgggtggcag ccaggcactg gtggaccgta tacgtctgca gggcctcaag      720
gacatgaccg gtgcggtgct ctgcgcccat gacgccgcac tgttgatgcg cggcatcaag      780
accctcaacc tgcgcatgga ccgccactgc gccaacgctc aggtgctggc cgagttcctc      840
gcccgtcagc cgcaggtgga gctgatccat taccggggcc tggcgagctt cccgcagtac      900
accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc      960
ggcatcggtg ccgggcgctg tttcatgaac gccctgcaac tgttcagccg cgcggtgagc     1020
ctgggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc     1080
ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcgtttgtc ggtggggctg     1140
gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgccctga     1197
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<210> 29

<211> 1197

<212> DNA

<213> Artificial Sequence

<220>

<223> Methionine gamma-lyase gene derived from *Pseudomonas putida* having all rare arginine, leucine, isoleucine, and proline codons replaced

aced with respective corresponding codons found most commonly in
E. coli

<400> 29
atgcacggct ccaacaagct cccaggattt gccacccgcg ccattcacca tggctacgac 60
ccgcaggacc acggcggcgc actggtgcca ccggtctacc agaccgacgac gttcaccttc 120
ccgaccgtgg aatacggcgc tgcgtgcttt gccggcgagc aggcggggca tttctacagc 180
cgcatctcca acccgaccct caacctgctg gaagcacgca tggcctcgct ggaaggcggc 240
gaggccgggc tggcgctggc ctcgggcatg ggggcgatca cgtccacgct gtggacactg 300
ctgcgcccgg gtgacgaggt gctgctgggc aacaccctgt acggctgcac ctttgccctc 360
ctgcaccacg gcatcggcga gttcggggtc aagctgcgcc atgtggacat ggccgacctg 420
caggcactgg aggcggccat gacgccggcc acccgtgtga tctatttcga gtcgccggcc 480
aaccgaaca tgcacatggc cgatatcgcc ggcgtggcga agattgcacg caagcacggc 540
gcgaccgtgg tggctgacaa cacctactgc acgccgtacc tgcaacgtcc actggagctg 600
ggcgccgacc tgggtggtgca ttcggccacc aagtacctga gcggccatgg cgacatcact 660
gctggcattg tgggtggcag ccaggcactg gtggaccgta tccgtctgca gggcctcaag 720
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accctggccc gccagcagat gagccagccg ggcggcatga tcgccttcga actcaagggc 960
ggcatcggtg ccgggcgctg tttcatgaac gccctgcaac tgttcagccg cgcggtgagc 1020
ctgggcgatg ccgagtcgct ggcgcagcac ccggcaagca tgactcattc cagctatacc 1080
ccagaggagc gtgcgcatta cggcatctcc gaggggctgg tgcgtttgtc ggtggggctg 1140
gaagacatcg acgacctgct ggccgatgtg caacaggcac tcaaggcgag tgccctga 1197

<210> 30
<211> 1200
<212> DNA
<213> Artificial Sequence

<220>
<223> Methionine gamma-lyase gene derived from Pseudomonas putida havin
g all codons replaced with respective corresponding codons found
most commonly in E. coli

<400> 30
atgggtcacg gctccaacaa actgccgggt tttgctaccc gtgctatcca ccacggctac 60

gacccgcagg accacggcgg cgcactggtt ccgccggttt accagaccgc gaccttcacc	120
ttcccgaccg ttgaatacgg cgctgcgtgc tttgctggcg aacaggctgg tcacttctac	180
tcccgatatct ccaacccgac cctgaacctg ctggaagcac gtatggcttc cctggaaggc	240
ggcgaagctg gtctggcgct ggcttcgggc atgggtgcga tcacctccac cctgtggacc	300
ctgctgcgtc cgggtgacga agttctgctg ggcaacaccc tgtacggctg cacctttgct	360
ttcctgcacc acggcatcgg cgaattcggg gttaagctgc gtcacgttga catggctgac	420
ctgcaggcac tggaagcggc tatgaccccg gctaccctg ttatctactt cgaatccccg	480
gctaaccga acatgcacat ggctgaaatc gctggcggtg cgaagatcgc acgtaagcac	540
ggcgcgaccg ttgttggtga caacacctac tgcaccccg acctgcaacg tccgctggaa	600
ctgggcgctg acctggttgt tcaactcgt accaagtacc tgtccggcca cggcgacatc	660
actgctggca tcgttggttg ctcccaggca ctggttgacc gtatccgtct gcaaggcctg	720
aaggacatga ccggtgcggt tctgtccccg cagcagctg cactgctgat gcgtggcatc	780
aagaccctga acctgcgtat ggaccgtcac tgcgctaacg ctcaggttct ggctgaattc	840
ctggctcgtc agccgcaggt tgaactgac cactaccgg gcctggcgtc cttcccgcag	900
tacaccctgg ctgctcagca gatgtcccag ccggggcgga tgatcgcttt cgaactgaag	960
ggcggcatcg gtgctggctg tcgtttcatg aacgctctgc agctgttct cctgcggtt	1020
tccttgggcg aagctgaatc cctggcgag caccggcat ccatgactca ctctcctac	1080
accccggaag aacgtgcgca ctacggcatc tccgaaggtc tggttcgtct gtcggttggt	1140
ctggaagaca tcgacgacct gctggctgaa gttcagcagg cactgaaggc gagtgttga	1200

<210> 31
 <211> 972
 <212> DNA
 <213> *Sporidiobolus salmonicolor*

<400> 31	
atggctggca ctactaccct caacactggc gcttccctcg agctcgtcgg ctacggcacg	60
tggcaggcag caccgggcga ggtgggccag ggcgtcaagg tcgccatcga gactggatac	120
cgtcacctcg accttgccaa ggtctactcg aaccaacctg aggttggtgc cgccatcaag	180
gaggctggcg tcaagcgcgga ggacctcttc atcacctcga agctctggaa caactcgcac	240
cgcccgagc aggtcgagcc tgcccttgac gacacctca aggagctcgg cctcgagtac	300
ctcgaccttt acctcattca ctggcccgtc gcgttcccgc ccgagggcga catcaccag	360

aacctcttcc cgaaggccaa cgacaaggag gtcaagctcg acctggaggt cagcctcgtc 420
 gacacgtgga aggcgatggt caagcttctc gacactggca aggtcaaggc gatcggcggt 480
 tccaacttcg acgcgaagat ggtcgacgcc atcatcgagg ctaccggcgt gacccccctcc 540
 gtcaaccaga tcgagcggtca ccctctcctt ctccagcccg agtcatcgc ccaccacaag 600
 gccagaaca ttcacattac cgcatactct cctctcggtta acaacaccgt cggcgcgcct 660
 cttcttgtcc agcacccgga gatcaagcgc atcgccgaga agaacggctg cacgcccgtc 720
 caggtcctca ttgctgggc catcgttggc ggccactcgg ttatcccaa gtcggtcacc 780
 ccctcccgca ttggcgagaa cttcaagcag gtctcgctct cgcaggagga cgtcgatgcc 840
 gtcagcaagc tcggcgaggg ttggggcgc aggcgtaca acatccctg cacgtactcg 900
 cccaagtggg acatcaacgt ctttggcgag gaggacgaga agtcgtgcaa gaacgccgtg 960
 aagatcaagt ag 972

<210> 32
 <211> 322
 <212> PRT
 <213> Sporidiobolus salmonicolor

<400> 32

Met Val Gly Thr Thr Thr Leu Asn Thr Gly Ala Ser Leu Glu Leu Val
 1 5 10 15

Gly Tyr Gly Thr Trp Gln Ala Ala Pro Gly Glu Val Gly Gln Gly Val
 20 25 30

Lys Val Ala Ile Glu Thr Gly Tyr Arg His Leu Asp Leu Ala Lys Val
 35 40 45

Tyr Ser Asn Gln Pro Glu Val Gly Ala Ala Ile Lys Glu Ala Gly Val
 50 55 60

Lys Arg Glu Asp Leu Phe Ile Thr Ser Lys Leu Trp Asn Asn Ser His
 65 70 75 80

Arg Pro Glu Gln Val Glu Pro Ala Leu Asp Asp Thr Leu Lys Glu Leu
 85 90 95

Gly Leu Glu Tyr Leu Asp Leu Tyr Leu Ile Trp Pro Val Ala Phe Pro
 100 105 110

Pro Glu Gly Asp Ile Thr Gln Asn Leu Phe Pro Lys Ala Asn Asp Lys
115 120 125

Glu Val Lys Leu Asp Leu Glu Val Ser Leu Val Asp Thr Trp Lys Ala
130 135 140

Met Val Lys Leu Leu Asp Thr Gly Lys Val Lys Ala Ile Gly Val Ser
145 150 155 160

Asn Phe Asp Ala Lys Met Val Asp Ala Ile Ile Glu Ala Thr Gly Val
165 170 175

Thr Pro Ser Val Asn Gln Ile Glu Arg His Pro Leu Leu Leu Gln Pro
180 185 190

Glu Leu Ile Ala His His Lys Ala Lys Asn Ile His Ile Thr Ala Tyr
195 200 205

Ser Pro Leu Gly Asn Asn Thr Val Gly Ala Pro Leu Leu Val Gln His
210 215 220

Pro Glu Ile Lys Arg Ile Ala Glu Lys Asn Gly Cys Thr Pro Ala Gln
225 230 235 240

Val Leu Ile Ala Trp Ala Ile Val Gly Gly His Ser Val Ile Pro Lys
245 250 255

Ser Val Thr Pro Ser Arg Ile Gly Glu Asn Phe Lys Gln Val Ser Leu
260 265 270

Ser Gln Glu Asp Val Asp Ala Val Ser Lys Leu Gly Glu Gly Ser Gly
275 280 285

Arg Arg Arg Tyr Asn Ile Pro Cys Thr Tyr Ser Pro Lys Trp Asp Ile
290 295 300

Asn Val Phe Gly Glu Glu Asp Glu Lys Ser Cys Lys Asn Ala Val Lys
305 310 315 320

Ile Lys

<210> 33
 <211> 972
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic gene derived from *Sporidiobolus salmonicolor* NADPH-Dependent Aldehyde Reductase 1, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding

<400> 33
 atggttggtga ctactactct gaacactggt gcatctctgg aactggtagg ttatggtact 60
 tggcaagctg ctccgggcga agtaggtcaa ggtgtaaaag tagctatcga aactggttat 120
 cgtcatctgg atctggcaaa agtatactct aaccagccgg aagtaggtgc agcaatcaag 180
 gaagctggcg ttaaactgga ggatctgttt atcacttcta aactgtggaa caactcccac 240
 cgtccggaac aggtagaacc ggctctggat gatactctga aagaactggg cctggagtat 300
 ctggacctgt acctgatcca ctggccggta gcatttcgcg cggaaggtga tatcactcag 360
 aacctgttcc cgaaagctaa cgataaagaa gtaaaactgg acctggaagt ttctctggta 420
 gacacttgga aagcaatggt aaaactgctg gatactggta aagttaaagc tatcggtggt 480
 tccaactttg acgcaaaaat ggttgacgct atcatcgaag caactggcgt aactccgtct 540
 gttaaccaga tcgaacgtca cccgctgctg ctgcagccag agctgatcgc acaccacaaa 600
 gctaaaaaca tccacatcac cgcatactcc ccgctgggta acaacaccgt aggcgcaccg 660
 ctgctgggtac aacacccgga aatcaaactg atcgtgaaa aaaacggctg tactccggct 720
 caggtactga tcgcatgggc tatcgtaggt ggtcattctg ttatcccga atccgtaact 780
 ccgtctcgta ttggcgaaaa cttcaaacag gtttctctgt ctgaggaaga tgttgatgct 840
 gtttctaagc tgggcgaagg ttccggctcg cgtcggtata acatcccgtg cacttattcc 900
 ccgaagtggg atatcaactg ttccggtgaa gaagatgaaa aatcctgtaa aaacgctggt 960
 aaaatcaaat aa 972

<210> 34
 <211> 1032
 <212> DNA
 <213> *Sporidiobolus salmonicolor*

<400> 34
 atggcAAAAA tcgacaacgc tgtgcttccc gagggctcgc tcgtgctcgt caccggcgcc 60
 aacggcttcg tcgcttcgca cgtcgtcgaa cagctccttg aacacggtta caaggctcgt 120

ggtacggctc gtagtgctc caaacttgcc aacctgcaga agcgctggga tgccaagtac 180
 cccggtcgct tcgagacggc cgtggtcgag gacatgctca aacagggagc ttacgacgaa 240
 gtgatcaagg gcgccgcccg agttgcgcac atcgcttccg tcgtgtcctt ctcgaacaag 300
 tacgacgagg ttgtcacccc cgccatcgga ggcacctca acgctctccg tgccgcccgt 360
 gccacgccct ctgtcaagcg cttcgtcctc acctcctcga ccgtttcagc gcttatcccc 420
 aagccgaatg tcgaggggat ctacctcgac gagaagtctt ggaacctcga gagcatcgac 480
 aaggccaaga ctctccctga aagcgacccc cagaagtcgc tctgggtcta cgccgcgagc 540
 aagaccgagg cggagcttgc cgcttgga aa ttcatggacg agaacaagcc gcacttcacc 600
 ctcaacgccg tcctcccaa ctacacgatt gggacgatct tcgaccccga gacctcagtc 660
 ggctcgactt cgggctggat gatgagtctc ttcaatggcg aagtttcccc cgccctcgct 720
 ctgatgcccc ctcagtacta cgtgtcggcc gtcgacattg gtctcctgca cctcgggtgc 780
 ttggttctgc ccagatcga gcgcccgcgc gtctacggca ccgcccgcac gttcgactgg 840
 aacacggtcc tcgcgacgtt ccgcaagctg tacccgagca agacgttccc ggccgacttc 900
 cccgaccagg gccaggacct ctccaagtcc gacacggccc cgagcctcga gatcctcaag 960
 agtttgggca ggcccgggtg gaggtcgatc gaggagagca tcaaggacct cgtcggctcc 1020
 gaaaccgctt ga 1032

<210> 35
 <211> 343
 <212> PRT
 <213> *Sporidiobolus salmonicolor*

<400> 35

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
 1 5 10 15

Val Thr Gly Ala Asn Gly Phe Val Ala Ser His Val Val Glu Gln Leu
 20 25 30

Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
 35 40 45

Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
 50 55 60

Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65 70 75 80

Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
85 90 95

Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
100 105 110

Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115 120 125

Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
130 135 140

Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145 150 155 160

Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165 170 175

Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180 185 190

Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
195 200 205

Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
210 215 220

Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
225 230 235 240

Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
245 250 255

His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
260 265 270

Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
275 280 285

Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly

290

295

300

Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
 305 310 315 320

Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
 325 330 335

Leu Val Gly Ser Glu Thr Ala
 340

<210> 36
 <211> 1032
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic gene derived from *Sporidiobolus salmonicolor* NADPH-Dependent Aldehyde Reductase 2, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding, and an ala to gly mutation at amino acid position 2

<400> 36
 atggctaaaa tcgataacgc agttctgccg gaagggtccc tggttctggt taccggtgct 60
 aacggtttcg ttggttccca cgttgttgaa cagctgctgg aacacggtta caaagttcgt 120
 ggtaccgctc gttccgcttc caaactggct aacctgcaga aacggtggga cgctaaatac 180
 ccgggtcggt tcgaaaccgc tggtgttgaa gacatgctga aacagggtgc ttacgacgaa 240
 gttatcaaag gtgctgctgg tggtgctcac atcgcttcg ttgtttcctt ctccaacaaa 300
 tacgacgaag ttgttaccgc ggctatcggt ggtaccctga acgctctgcg tgctgctgct 360
 gctaccccg tctgttaaagc tttcggtctg acctcctcca ccgtttccgc tctgatcccg 420
 aaaccgaacg ttgaaggtat ctacctggac gaaaaatcct ggaacctgga atccatcgac 480
 aaagctaaaa ccctgccgga atccgacccg cagaaatccc tgtgggtata cgctgcatcc 540
 aagaccgaag ctgaactggc tgcattggaaa tttatggatg agaacaagcc acacttcact 600
 ctgaacgctg tactgccaaa ctacactatt ggcactatct tcgatccgga aactcagtcc 660
 ggttccacct ccggttggtat gatgtccctg tttaacggcg aggtttcccc ggctctggct 720
 ctgatgccac cgcagtacta cgtttccgct gttgatattg gcctgctgca cctggggtgc 780
 ctggttctgc cacaaatcga acgtcgtcgt gtttacggta ctgctggtac tttcgattgg 840
 aacaccgttc tggtacatt ccgtaaacgt taccggtcca aaaccttccc ggctgacttc 900

ccagatcaag gtcaggacct gtctaaattc gacaccgctc cgtccctgga aattctgaaa 960
tctctggggtc gccaggttg gcgttccatc gaagaatcca tcaaagacct ggttggttcc 1020
gaaaccgctt aa 1032

<210> 37
<211> 343
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic protein derived from Sporidiobolus salmonicolor NADPH-D
dependent Aldehyde Reductase 2, having an ala to gly mutation at a
mino acid position 2

<400> 37

Met Ala Lys Ile Asp Asn Ala Val Leu Pro Glu Gly Ser Leu Val Leu
1 5 10 15

Val Thr Gly Ala Asn Gly Phe Val Gly Ser His Val Val Glu Gln Leu
20 25 30

Leu Glu His Gly Tyr Lys Val Arg Gly Thr Ala Arg Ser Ala Ser Lys
35 40 45

Leu Ala Asn Leu Gln Lys Arg Trp Asp Ala Lys Tyr Pro Gly Arg Phe
50 55 60

Glu Thr Ala Val Val Glu Asp Met Leu Lys Gln Gly Ala Tyr Asp Glu
65 70 75 80

Val Ile Lys Gly Ala Ala Gly Val Ala His Ile Ala Ser Val Val Ser
85 90 95

Phe Ser Asn Lys Tyr Asp Glu Val Val Thr Pro Ala Ile Gly Gly Thr
100 105 110

Leu Asn Ala Leu Arg Ala Ala Ala Thr Pro Ser Val Lys Arg Phe
115 120 125

Val Leu Thr Ser Ser Thr Val Ser Ala Leu Ile Pro Lys Pro Asn Val
130 135 140

Glu Gly Ile Tyr Leu Asp Glu Lys Ser Trp Asn Leu Glu Ser Ile Asp
145 150 155 160

Lys Ala Lys Thr Leu Pro Glu Ser Asp Pro Gln Lys Ser Leu Trp Val
165 170 175

Tyr Ala Ala Ser Lys Thr Glu Ala Glu Leu Ala Ala Trp Lys Phe Met
180 185 190

Asp Glu Asn Lys Pro His Phe Thr Leu Asn Ala Val Leu Pro Asn Tyr
195 200 205

Thr Ile Gly Thr Ile Phe Asp Pro Glu Thr Gln Ser Gly Ser Thr Ser
210 215 220

Gly Trp Met Met Ser Leu Phe Asn Gly Glu Val Ser Pro Ala Leu Ala
225 230 235 240

Leu Met Pro Pro Gln Tyr Tyr Val Ser Ala Val Asp Ile Gly Leu Leu
245 250 255

His Leu Gly Cys Leu Val Leu Pro Gln Ile Glu Arg Arg Arg Val Tyr
260 265 270

Gly Thr Ala Gly Thr Phe Asp Trp Asn Thr Val Leu Ala Thr Phe Arg
275 280 285

Lys Leu Tyr Pro Ser Lys Thr Phe Pro Ala Asp Phe Pro Asp Gln Gly
290 295 300

Gln Asp Leu Ser Lys Phe Asp Thr Ala Pro Ser Leu Glu Ile Leu Lys
305 310 315 320

Ser Leu Gly Arg Pro Gly Trp Arg Ser Ile Glu Glu Ser Ile Lys Asp
325 330 335

Leu Val Gly Ser Glu Thr Ala
340

<210> 38
<211> 942
<212> DNA
<213> Saccharomyces cerevisiae

<400> 38
atgggtcctg ctacgttaaa gaattcttct gctacattaa aactaaatac tgggtgcctcc

attccagtgt tgggtttcgg cacttggcgt tccgttgaca ataacggtta ccattctgta 120
 attgcagctt tgaaagctgg atacagacac attgatgctg cggctatcta tttgaatgaa 180
 gaagaagttg gcagggctat taaagattcc ggagtcctc gtgaggaaat ttttattact 240
 actaagcttt ggggtacgga acaacgtgat ccggaagctg ctctaaacaa gtctttgaaa 300
 agactaggct tggattatgt tgacctatat ctgatgcatt ggccagtgcc tttgaaaacc 360
 gacagagtta ctgatggtaa cgttctgtgc attccaacat tagaagatgg cactgttgac 420
 atcgatacta aggaatggaa ttttatcaag acgtgggagt tgatgcaaga gttgccaaag 480
 acggggcaaaa ctaaagccgt tgggtgtctct aatttttcta ttaacaacat taaagaatta 540
 ttagaatctc caaataacaa ggtggtacca gctactaatc aaattgaaat tcattccattg 600
 ctaccacaag acgaattgat tgccttttgt aaggaaaagg gtattgttgt tgaagcctac 660
 tcaccatttg ggagtgctaa tgctccttta ctaaaagagc aagcaattat tgatatggct 720
 aaaaagcacg gcgttgagcc agcacagctt attatcagtt ggagtattca aagaggctac 780
 gttgttctgg ccaaatcggt taatcctgaa agaattgtat ccaattttaa gattttcact 840
 ctgcctgagg atgatttcaa gactattagt aacctatcca aagtgcattg tacaaagaga 900
 gtcgttgata tgaagtgggg atccttccca attttccaat ga 942

<210> 39
 <211> 313
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 39

Met Gly Pro Ala Thr Leu Lys Asn Ser Ser Ala Thr Leu Lys Leu Asn
 1 5 10 15

Thr Gly Ala Ser Ile Pro Val Leu Gly Phe Gly Thr Trp Arg Ser Val
 20 25 30

Asp Asn Asn Gly Tyr His Ser Val Ile Ala Ala Leu Lys Ala Gly Tyr
 35 40 45

Arg His Ile Asp Ala Ala Ala Ile Tyr Leu Asn Glu Glu Glu Val Gly
 50 55 60

Arg Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Ile Thr
 65 70 75 80

Thr Lys Leu Trp Gly Thr Glu Gln Arg Asp Pro Glu Ala Ala Leu Asn
85 90 95

Lys Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met
100 105 110

His Trp Pro Val Pro Leu Lys Thr Asp Arg Val Thr Asp Gly Asn Val
115 120 125

Leu Cys Ile Pro Thr Leu Glu Asp Gly Thr Val Asp Ile Asp Thr Lys
130 135 140

Glu Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys
145 150 155 160

Thr Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn
165 170 175

Ile Lys Glu Leu Leu Glu Ser Pro Asn Asn Lys Val Val Pro Ala Thr
180 185 190

Asn Gln Ile Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Ala
195 200 205

Phe Cys Lys Glu Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Phe Gly
210 215 220

Ser Ala Asn Ala Pro Leu Leu Lys Glu Gln Ala Ile Ile Asp Met Ala
225 230 235 240

Lys Lys His Gly Val Glu Pro Ala Gln Leu Ile Ile Ser Trp Ser Ile
245 250 255

Gln Arg Gly Tyr Val Val Leu Ala Lys Ser Val Asn Pro Glu Arg Ile
260 265 270

Val Ser Asn Phe Lys Ile Phe Thr Leu Pro Glu Asp Asp Phe Lys Thr
275 280 285

Ile Ser Asn Leu Ser Lys Val His Gly Thr Lys Arg Val Val Asp Met
290 295 300

Lys Trp Gly Ser Phe Pro Ile Phe Gln
305 310

<210> 40
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic gene derived from *Saccharomyces cerevisiae* YPR1 putative reductase, having glycine codon inserted after the initiating methionine codon

<400> 40
atgggtccgg caactctgaa gaactcttct gcaactctga aactgaacac tgggtgcatct 60
atccccgttc tgggttttcgg tacttggcgt tctgttgaca acaacggtta ccactccggt 120
atcgcagcac tgaaagcagg ttaccgtcac atcgacgcag cagcaatcta cctgaacgaa 180
gaagaagtag gtcgtgcaat caaagactcc ggtgttccgc gtgaagaaat ctttatcact 240
actaaactgt ggggtactga acagcgtgac ccggaagcag cactgaacaa atctctgaaa 300
cgtctgggtc tggactacgt agacctgtac ctgatgcact ggccggtacc gctgaaaact 360
gaccgtgtta ctgatggtaa cgttctgtgt attccgactc tggaagacgg tactgtagac 420
atcgacacta aggaatggaa cttcatcaag acttgggaac tgatgcagga actgccgaaa 480
actggtaaaa ctaaagcagt aggtgtttcc aacttctcta tcaacaacat caaagaactg 540
ctggaatctc cgaacaacaa agtagtaccg gcaactaacc agatcgaaat ccaccgctg 600
ctgccgcagg acgaactgat cgcattctgc aaagagaaaag gtatcgtagt agaagcatac 660
tctccgttcg gctctgcaaa cgcaccgctg ctgaaagaac aggcaatcat cgacatggca 720
aagaaacacg gtgtagaacc ggcacagctg atcatctctt ggtctatcca gcgtgggttac 780
gtagtactgg caaaatctgt aaaccgggaa cgtatcgtat ctaacttcaa aatcttcact 840
ctgccggaag acgacttcaa aactatctct aacctgtcca aagttcacgg tactaaacgt 900
gtagtagaca tgaaatgggg ttctttcccg atcttccagt aa 942

<210> 41
<211> 939
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 41
atgcctgcta ctttacatga ttctacgaaa atcctttctc taaatactgg agcccaaadc 60

cctcaaatag gtttaggtac gtggcagtcg aaagagaacg atgcttataa ggctgtttta 120
accgctttga aagatggcta cgcacacatt gatactgctg ctatttaccg taatgaagac 180
caagtcgggc aagccatcaa ggattcaggt gttcctcggg aagaaatctt tgttactaca 240
aagttatggg gtacacaaca ccacgaacct gaagtagcgc tggatcaatc actaaagagg 300
ttaggattgg actacgtaga cttatatttg atgcattggc ctgccagatt agatccagcc 360
tacatcaaaa atgaagacat cttgagtgtg ccaacaaaga aggatgggtc tcgtgcagtg 420
gatatcacca attggaattt catcaaaacc tgggaattaa tgcaggaact accaaagact 480
ggtaaaacta aggcggttg agtctccaac ttttctataa ataacctgaa agatctatta 540
gcatctcaag gtaataagct tacgccagct gctaaccaag tcgaaataca tccattacta 600
cctcaagacg aattgattaa tttttgtaaa agtaaaggca ttgtgggttg agcttattct 660
ccgttaggta gtaccgatgc tccactattg aaggaaccgg ttatccttga aattgcgaag 720
aaaaataacg ttcaaccgg acacgttggt attagctggc acgtccaaag aggttatggt 780
gtcttgccaa aatctgtgaa tcccgatcga atcaaaacga acaggaaaat atttactttg 840
tctactgagg actttgaagc tatcaataac atatcgaagg aaaagggcga aaaaaggggt 900
gtacatccaa attggtctcc tttcgaagta ttcaagtaa 939

<210> 42
<211> 312
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 42

Met Pro Ala Thr Leu His Asp Ser Thr Lys Ile Leu Ser Leu Asn Thr
1 5 10 15

Gly Ala Gln Ile Pro Gln Ile Gly Leu Gly Thr Trp Gln Ser Lys Glu
20 25 30

Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr Arg
35 40 45

His Ile Asp Thr Ala Ala Ile Tyr Arg Asn Glu Asp Gln Val Gly Gln
50 55 60

Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Val Thr Thr
65 70 75 80

Lys Leu Trp Cys Thr Gln His His Glu Pro Glu Val Ala Leu Asp Gln
85 90 95

Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met His
100 105 110

Trp Pro Ala Arg Leu Asp Pro Ala Tyr Ile Lys Asn Glu Asp Ile Leu
115 120 125

Ser Val Pro Thr Lys Lys Asp Gly Ser Arg Ala Val Asp Ile Thr Asn
130 135 140

Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys Thr
145 150 155 160

Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn Leu
165 170 175

Lys Asp Leu Leu Ala Ser Gln Gly Asn Lys Leu Thr Pro Ala Ala Asn
180 185 190

Gln Val Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Asn Phe
195 200 205

Cys Lys Ser Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Leu Gly Ser
210 215 220

Thr Asp Ala Pro Leu Leu Lys Glu Pro Val Ile Leu Glu Ile Ala Lys
225 230 235 240

Lys Asn Asn Val Gln Pro Gly His Val Val Ile Ser Trp His Val Gln
245 250 255

Arg Gly Tyr Val Val Leu Pro Lys Ser Val Asn Pro Asp Arg Ile Lys
260 265 270

Thr Asn Arg Lys Ile Phe Thr Leu Ser Thr Glu Asp Phe Glu Ala Ile
275 280 285

Asn Asn Ile Ser Lys Glu Lys Gly Glu Lys Arg Val Val His Pro Asn
290 295 300

Trp Ser Pro Phe Glu Val Phe Lys
305 310

<210> 43
<211> 942
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic gene derived from *Saccharomyces cerevisiae* GCY1 reductase, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding, and a ggc insertion after the initiating atg

<400> 43
atgggcccag ctactctgca cgactctacc aaaattctgt ctctgaacac cgggtgctcaa 60
atccccgaaa tcggcctggg tacttggcaa tctaaagaaa acgacgcata caaggctggt 120
ctgactgctc tgaaggatgg ctatcgtcac attgatactg ctgctattta tcgtaacgag 180
gaccaggtag gtcaggcaat caaggactct ggcgttcgcg gtgaggaaat cttcgtaact 240
accaaactgt ggtgcactca gcatcatgaa ccggaagtag cactggatca atctctgaag 300
cgtctgggtc tggactatgt tgatctgtac ctgatgcatt ggccggcgcg cctggacceca 360
gcgtatatta aaaacgaaga tctctgtct gttccgacta agaaagacgg ctctcgtgct 420
gttgacatca ctaactggaa cttcatcaag acctgggaac tgatgcagga actgccgaag 480
actggtaaaa ctaaagctgt tggcgtatct aacttctcca tcaacaacct gaaggacctg 540
ctggcatccc agggcaacaa gctgactccg gctgctaacc aagtagagat ccaccgctg 600
ctgccgcagg acgaactgat caacttctgt aaatctaaag gcattgtagt tgaagcatat 660
tctccgctgg gttctaccga tgcgccactg ctgaaagagc cggtaatcct ggagatcgcg 720
aagaaaaaca acgtacaacc aggtcatgta gtaatctctt ggcacgtaca gcgcggctac 780
gtagttctgc cgaagtctgt aaaccgggat cgtatcaaaa ctaaccgtaa aatctttacc 840
ctgtccaccg aagatttcga agcaatcaac aacatctcca aggaaaaggg cgagaaacgt 900
gtagttcacc caaactggtc cccgtttgaa gtattcaagt aa 942

<210> 44
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic protein derived from *Saccharomyces cerevisiae* GCY1 reductase, having a glycine inserted at position 2 in the amino acid

sequence

<400> 44

Met Gly Pro Ala Thr Leu His Asp Ser Thr Lys Ile Leu Ser Leu Asn
1 5 10 15

Thr Gly Ala Gln Ile Pro Gln Ile Gly Leu Gly Thr Trp Gln Ser Lys
20 25 30

Glu Asn Asp Ala Tyr Lys Ala Val Leu Thr Ala Leu Lys Asp Gly Tyr
35 40 45

Arg His Ile Asp Thr Ala Ala Ile Tyr Arg Asn Glu Asp Gln Val Gly
50 55 60

Gln Ala Ile Lys Asp Ser Gly Val Pro Arg Glu Glu Ile Phe Val Thr
65 70 75 80

Thr Lys Leu Trp Cys Thr Gln His His Glu Pro Glu Val Ala Leu Asp
85 90 95

Gln Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Leu Tyr Leu Met
100 105 110

His Trp Pro Ala Arg Leu Asp Pro Ala Tyr Ile Lys Asn Glu Asp Ile
115 120 125

Leu Ser Val Pro Thr Lys Lys Asp Gly Ser Arg Ala Val Asp Ile Thr
130 135 140

Asn Trp Asn Phe Ile Lys Thr Trp Glu Leu Met Gln Glu Leu Pro Lys
145 150 155 160

Thr Gly Lys Thr Lys Ala Val Gly Val Ser Asn Phe Ser Ile Asn Asn
165 170 175

Leu Lys Asp Leu Leu Ala Ser Gln Gly Asn Lys Leu Thr Pro Ala Ala
180 185 190

Asn Gln Val Glu Ile His Pro Leu Leu Pro Gln Asp Glu Leu Ile Asn
195 200 205

Phe Cys Lys Ser Lys Gly Ile Val Val Glu Ala Tyr Ser Pro Leu Gly

210

215

220

Ser Thr Asp Ala Pro Leu Leu Lys Glu Pro Val Ile Leu Glu Ile Ala
 225 230 235 240

Lys Lys Asn Asn Val Gln Pro Gly His Val Val Ile Ser Trp His Val
 245 250 255

Gln Arg Gly Tyr Val Val Leu Pro Lys Ser Val Asn Pro Asp Arg Ile
 260 265 270

Lys Thr Asn Arg Lys Ile Phe Thr Leu Ser Thr Glu Asp Phe Glu Ala
 275 280 285

Ile Asn Asn Ile Ser Lys Glu Lys Gly Glu Lys Arg Val Val His Pro
 290 295 300

Asn Trp Ser Pro Phe Glu Val Phe Lys
 305 310

<210> 45
 <211> 1029
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 45
 atgtcagttt tcgtttcagg tgctaacggg ttcattgccc aacacattgt cgatctcctg 60
 ttgaaggaag actataaggt catcggttct gccagaagtc aagaaaaggc cgagaattta 120
 acggaggcct ttggtaacaa cccaaaattc tccatggaag ttgtcccaga catatctaag 180
 ctggacgcat ttgacctgtt tttccaaaag cacggcaagg atatcaagat agttctacat 240
 acggcctctc cattctgctt tgatatcact gacagtgaac gcgatttatt aattcctgct 300
 gtgaacggtg ttaaggggaat tctccactca attaaaaaat acgccgctga ttctgtagaa 360
 cgtgtagttc tcacctcttc ttatgcagct gtgttcgata tggcaaaaga aaacgataag 420
 tctttaacat ttaacgaaga atcctggaac ccagctacct gggagagttg ccaaagtgc 480
 ccagttaacg cctactgtgg ttctaagaag tttgctgaaa aagcagcttg ggaatttcta 540
 gaggagaata gagactctgt aaaattcgaa ttaactgccg ttaaccagct ttacgttttt 600
 ggtccgcaaa tgtttgacaa agatgtgaaa aaacacttga acacatcttg cgaactcgtc 660
 aacagcttga tgcatttatc accagaggac aagataccgg aactatttgg tggatacatt 720

gatgttcgtg atgttgcaaa ggctcattta gttgccttcc aaaagaggga aacaattggt 780
caaagactaa tcgtatcgga ggccagattt actatgcagg atgttctcga tatecttaac 840
gaagacttcc ctgttctaaa aggcaatatt ccagtgggga aaccagggtc tgggtgctacc 900
cataacaccc ttggtgctac tcttgataat aaaaagagta agaaattggt aggtttcaag 960
ttcaggaact tgaaagagac cattgacgac actgcctccc aaattttaaa atttgagggc 1020
agaatataa 1029

<210> 46
<211> 342
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 46

Met Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His Ile
1 5 10 15

Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala Arg
20 25 30

Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn Pro
35 40 45

Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala Phe
50 55 60

Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu His
65 70 75 80

Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp Leu
85 90 95

Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile Lys
100 105 110

Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Leu Thr Ser Ser Tyr
115 120 125

Ala Ala Val Phe Asp Met Ala Lys Glu Asn Asp Lys Ser Leu Thr Phe
130 135 140

Asn Glu Glu Ser Trp Asn Pro Ala Thr Trp Glu Ser Cys Gln Ser Asp

145		150		155		160
Pro Val Asn Ala Tyr Cys Gly Ser Lys Lys Phe Ala Glu Lys Ala Ala						
	165		170		175	
Trp Glu Phe Leu Glu Glu Asn Arg Asp Ser Val Lys Phe Glu Leu Thr						
	180		185		190	
Ala Val Asn Pro Val Tyr Val Phe Gly Pro Gln Met Phe Asp Lys Asp						
	195		200		205	
Val Lys Lys His Leu Asn Thr Ser Cys Glu Leu Val Asn Ser Leu Met						
	210		215		220	
His Leu Ser Pro Glu Asp Lys Ile Pro Glu Leu Phe Gly Gly Tyr Ile						
	225		230		235	240
Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln Lys Arg						
	245		250		255	
Glu Thr Ile Gly Gln Arg Leu Ile Val Ser Glu Ala Arg Phe Thr Met						
	260		265		270	
Gln Asp Val Leu Asp Ile Leu Asn Glu Asp Phe Pro Val Leu Lys Gly						
	275		280		285	
Asn Ile Pro Val Gly Lys Pro Gly Ser Gly Ala Thr His Asn Thr Leu						
	290		295		300	
Gly Ala Thr Leu Asp Asn Lys Lys Ser Lys Lys Leu Leu Gly Phe Lys						
	305		310		315	320
Phe Arg Asn Leu Lys Glu Thr Ile Asp Asp Thr Ala Ser Gln Ile Leu						
	325		330		335	
Lys Phe Glu Gly Arg Ile						
	340					

<210> 47
 <211> 1032
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Synthetic gene derived from *Saccharomyces cerevisiae* GRE2 reductase, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding, and a ggc insertion at position 2 in the amino acid sequence

```

<400> 47
atgggctctg tatttgatc tggcgctaac ggttttatcg ctcaacacat cgtcgatctg      60
ctgctgaaag aagattacaa agttatcggg tccgcacggt cccaggaaaa agctgaaaac      120
ctgactgaag catttggtaa caaccgaag ttctctatgg aagtagtacc ggacatttct      180
aaactggacg cattcgacca cgtattccaa aagcacggta aggatatcaa gatcgtactg      240
cacactgcat ctccattctg ttttgacatc actgattctg agcgcgacct gctgattccg      300
gctgttaacg gtgttaaagg tattctgcac tctattaaga aatatgctgc tgattccgta      360
gaacgcgtag ttctgacttc ctcttatgct gcagtattcg atatggctaa agagaacgac      420
aaatccctga cttttaacga agaatcttgg aaccgggcta cctgggaatc ttgccagtct      480
gaccgggtta acgcttattg tggctctaag aagtttgctg aaaaagctgc ttgggaattc      540
ctggaagaaa accgtgactc tgtaaagttc gagctgaccg ctgtaaaccg ggtatacggt      600
tttggcccg c agatgttcga taaagatgta aagaagcacc tgaacacttc ctgtgaactg      660
gtaaactctc tgatgcacct gtctccagaa gataaaatcc cggagctggt cggcggttac      720
atcgacgttc gtgacgtagc aaaagcacat ctggtagctt tccagaagcg tgagactatc      780
ggccagcgtc tgattgtttc cgaggctcgt ttcaccatgc aggatgttct ggatattctg      840
aacgaagact tcccgtact gaaaggtaac attccgggtg gtaaaccagg ctctggtgca      900
actcataaca ctctgggtgc aactctggat aacaagaagt ctaagaaact gctgggtttt      960
aaattccgta acctgaaaga aactattgac gacactgcat ctcagatcct gaaattcgaa     1020
ggtcgcatct aa                                           1032

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<210> 48
<211> 343
<212> PRT
<213> Artificial Sequence

```

<220>
 <223> Synthetic protein derived from *Saccharomyces cerevisiae* Gre2 reductase, having a glycine inserted at position 2 in the amino acid sequence

<400> 48

```

Met Gly Ser Val Phe Val Ser Gly Ala Asn Gly Phe Ile Ala Gln His
1           5           10           15

```

Ile Val Asp Leu Leu Leu Lys Glu Asp Tyr Lys Val Ile Gly Ser Ala
20 25 30

Arg Ser Gln Glu Lys Ala Glu Asn Leu Thr Glu Ala Phe Gly Asn Asn
35 40 45

Pro Lys Phe Ser Met Glu Val Val Pro Asp Ile Ser Lys Leu Asp Ala
50 55 60

Phe Asp His Val Phe Gln Lys His Gly Lys Asp Ile Lys Ile Val Leu
65 70 75 80

His Thr Ala Ser Pro Phe Cys Phe Asp Ile Thr Asp Ser Glu Arg Asp
85 90 95

Leu Leu Ile Pro Ala Val Asn Gly Val Lys Gly Ile Leu His Ser Ile
100 105 110

Lys Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Leu Thr Ser Ser
115 120 125

Tyr Ala Ala Val Phe Asp Met Ala Lys Glu Asn Asp Lys Ser Leu Thr
130 135 140

Phe Asn Glu Glu Ser Trp Asn Pro Ala Thr Trp Glu Ser Cys Gln Ser
145 150 155 160

Asp Pro Val Asn Ala Tyr Cys Gly Ser Lys Lys Phe Ala Glu Lys Ala
165 170 175

Ala Trp Glu Phe Leu Glu Glu Asn Arg Asp Ser Val Lys Phe Glu Leu
180 185 190

Thr Ala Val Asn Pro Val Tyr Val Phe Gly Pro Gln Met Phe Asp Lys
195 200 205

Asp Val Lys Lys His Leu Asn Thr Ser Cys Glu Leu Val Asn Ser Leu
210 215 220

Met His Leu Ser Pro Glu Asp Lys Ile Pro Glu Leu Phe Gly Gly Tyr
225 230 235 240

Ile Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln Lys
 245 250 255

Arg Glu Thr Ile Gly Gln Arg Leu Ile Val Ser Glu Ala Arg Phe Thr
 260 265 270

Met Gln Asp Val Leu Asp Ile Leu Asn Glu Asp Phe Pro Val Leu Lys
 275 280 285

Gly Asn Ile Pro Val Gly Lys Pro Gly Ser Gly Ala Thr His Asn Thr
 290 295 300

Leu Gly Ala Thr Leu Asp Asn Lys Lys Ser Lys Lys Leu Leu Gly Phe
 305 310 315 320

Lys Phe Arg Asn Leu Lys Glu Thr Ile Asp Asp Thr Ala Ser Gln Ile
 325 330 335

Leu Lys Phe Glu Gly Arg Ile
 340

<210> 49
 <211> 987
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Essentially encodes the native GRE3 reductase gene from *Saccharom yces cerevisiae*, but has a codon for isoleucine inserted after the initiating methionine codon to incorporate a restriction site

<400> 49
 atgatttctt cactgggttac tcttaataac ggtctgaaaa tgcccctagt cggcttaggg 60
 tgctggaaaa ttgacaaaaa agtctgtgcg aatcaaattt atgaagctat caaattaggc 120
 taccgtttat tcgatggtgc ttgcgactac ggcaacgaaa aggaagttgg tgaaggtatc 180
 aggaaagcca tctccgaagg tcttgtttct agaaaggata tatttggtgt ttcaaagtta 240
 tggacaatt ttcaccatcc tgatcatgta aaattagctt taaagaagac cttaagcgat 300
 atgggacttg attatttaga cctgtattat attcacttcc caatcgctt caaatatggt 360
 ccatttgaag agaaataccc tccaggattc tatacgggcg cagatgacga gaagaaaggt 420
 cacatcacgc aagcacatgt accaatcata gatacgtacc gggctctgga agaattgtgt 480
 gatgaaggct tgattaagtc tattggtggt tccaactttc aggggaagctt gattcaagat 540

ttattacgtg gttgtagaat caagcccgtg gctttgcaaa ttgaacacca tccttatttg 600
 actcaagaac acctagttga gttttgtaaa ttacacgata tccaagtagt tgcttactcc 660
 tccttcgggtc ctcaatcatt cattgagatg gacttacagt tggcaaaaac cagccaact 720
 ctgttcgaga atgatgtaat caagaagggtc tcacaaaacc atccaggcag taccacttcc 780
 caagtattgc ttagatgggc aactcagaga ggcattgccg tcattccaaa atcttccaag 840
 aaggaaaggt tacttgga cctagaaatc gaaaaaaagt tcactttaac ggagcaagaa 900
 ttgaaggata tttctgcact aaatgccaac atcagattta atgatccatg gacctgggtg 960
 gatggtaaat tccccacttt tgcctga 987

<210> 50
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Essentially encodes the native GRE3 reductase protein from *Saccharomyces cerevisiae*, but has an isoleucine inserted after the initiating methionine

<400> 50

Met Ile Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu
 1 5 10 15

Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln
 20 25 30

Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys
 35 40 45

Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile
 50 55 60

Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu
 65 70 75 80

Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys
 85 90 95

Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His
 100 105 110

Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro
115 120 125

Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu
130 135 140

Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val
145 150 155 160

Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser
165 170 175

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu
180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe
195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro
210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr
225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly
245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile
260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu
275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile
290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu
305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala
325

<210> 51
<211> 987
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic gene derived from *Saccharomyces cerevisiae* GRE3 reductase, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding, and a ggc codon insertion after the initiating atg

<400> 51
atgggctctt ctctggtaac tctgaacaac ggtctgaaaa tgccgctggt aggcctgggc 60
tgctggaaaa tcgataagaa agtatgtgct aaccaaattt atgaggctat caaactgggc 120
tatcgctgt tcgacgggtgc ttgcgactat ggtaacgaga aggaagttgg tgaaggcatc 180
cgtaaagcta tctctgaagg tctggtatct cgtaaggata tctttgtagt atctaagctg 240
tggaacaact ttcattcacc ggatcacgta aaactggcac tgaagaaaac cctgtctgat 300
atgggtctgg attatctgga tctgtactat atccacttcc cgatcgcat taaatacgta 360
ccgttcgaag aaaaatatcc gccgggcttt tacactgggtg cagacgacga aaagaagggt 420
cacatcactg aagctcacgt accgatcatc gacacttacc gtgctctgga ggaatgtgta 480
gacgaaggtc tgatcaaata tatcggtgta tctaacttcc agggttctct gatccaggat 540
ctgctgcgtg gttgccgtat caagccggtt gctctgcaaa ttgaacacca cccgtacctg 600
accaggaac acctgggtga attctgcaaa ctgcacgata tccaagtagt agcatactct 660
tctttcggtc cgcagtcttt catcgaaatg gacctgcagc tggctaagac caccctgact 720
ctgttcgaaa acgacgtaat caagaaagta tctcagaacc acccgggctc tactacctct 780
cagggtactgc tgcgttgggc tactcagcgt ggcacgcgtg ttatcccgaa atcttctaag 840
aaagaacgtc tgctgggtaa cctggaaatc gaaaagaaat tcaactctgac cgaacaggaa 900
ctgaaagata tctctgctct gaacgctaac atccgtttca acgatccgtg gacctggctg 960
gatggtaaat tcccgaacttt cgcttaa 987

<210> 52
<211> 328
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic protein derived from *Saccharomyces cerevisiae* Gre3 reductase, having a glycine inserted at position 2 in the amino acid sequence

<400> 52

Met Gly Ser Ser Leu Val Thr Leu Asn Asn Gly Leu Lys Met Pro Leu
1 5 10 15

Val Gly Leu Gly Cys Trp Lys Ile Asp Lys Lys Val Cys Ala Asn Gln
20 25 30

Ile Tyr Glu Ala Ile Lys Leu Gly Tyr Arg Leu Phe Asp Gly Ala Cys
35 40 45

Asp Tyr Gly Asn Glu Lys Glu Val Gly Glu Gly Ile Arg Lys Ala Ile
50 55 60

Ser Glu Gly Leu Val Ser Arg Lys Asp Ile Phe Val Val Ser Lys Leu
65 70 75 80

Trp Asn Asn Phe His His Pro Asp His Val Lys Leu Ala Leu Lys Lys
85 90 95

Thr Leu Ser Asp Met Gly Leu Asp Tyr Leu Asp Leu Tyr Tyr Ile His
100 105 110

Phe Pro Ile Ala Phe Lys Tyr Val Pro Phe Glu Glu Lys Tyr Pro Pro
115 120 125

Gly Phe Tyr Thr Gly Ala Asp Asp Glu Lys Lys Gly His Ile Thr Glu
130 135 140

Ala His Val Pro Ile Ile Asp Thr Tyr Arg Ala Leu Glu Glu Cys Val
145 150 155 160

Asp Glu Gly Leu Ile Lys Ser Ile Gly Val Ser Asn Phe Gln Gly Ser
165 170 175

Leu Ile Gln Asp Leu Leu Arg Gly Cys Arg Ile Lys Pro Val Ala Leu
180 185 190

Gln Ile Glu His His Pro Tyr Leu Thr Gln Glu His Leu Val Glu Phe
195 200 205

Cys Lys Leu His Asp Ile Gln Val Val Ala Tyr Ser Ser Phe Gly Pro
210 215 220

Gln Ser Phe Ile Glu Met Asp Leu Gln Leu Ala Lys Thr Thr Pro Thr
 225 230 235 240

Leu Phe Glu Asn Asp Val Ile Lys Lys Val Ser Gln Asn His Pro Gly
 245 250 255

Ser Thr Thr Ser Gln Val Leu Leu Arg Trp Ala Thr Gln Arg Gly Ile
 260 265 270

Ala Val Ile Pro Lys Ser Ser Lys Lys Glu Arg Leu Leu Gly Asn Leu
 275 280 285

Glu Ile Glu Lys Lys Phe Thr Leu Thr Glu Gln Glu Leu Lys Asp Ile
 290 295 300

Ser Ala Leu Asn Ala Asn Ile Arg Phe Asn Asp Pro Trp Thr Trp Leu
 305 310 315 320

Asp Gly Lys Phe Pro Thr Phe Ala
 325

<210> 53
 <211> 1461
 <212> DNA
 <213> Sus scrofa

<400> 53
 atgaatgcc a gcgatttccg tcgacgcggc aaagaaatgg tggattacat ggcggattac 60
 ctggaaggca tcgaaggtcg tcaggtgtac ccggatgtgc agccggggta cctgcgtccg 120
 ctgatcccg cgaccgcccc gcaggaaccg gataccttcg aagatatact gcaggatgtg 180
 gaaaaaatca tcatgccggg ggtgaccac tggcacagcc cgtacttctt cgcgtacttc 240
 ccgaccgcca gcagctaccc ggcgatgctg gcggatatgc tgtgcggtgc gatcggatgc 300
 atcggtttca gctgggcggc tagcccggcg tgcaccgaac tcgagaccgt gatgatggat 360
 tggctgggca aaatgctcca gcttcggaa gcgttcctgg cgggcgaagc cggatgaaggc 420
 ggcggcgtga tccagggtag cgccagcgaa gccaccctgg tggcgtgct ggcggcgcgt 480
 accaaagtgg tgcgacgtct gcaagcggcg agcccgggcc tgaccaggg cgcgggtgctg 540
 gaaaaactag tggcgtacgc gaggatcag gcgcacagca gcgtggaacg tgccggcctg 600
 atcggcggcg tgaaactgaa agcgatccc agcgatggca aattcgcgat gcgtgcgagc 660

gcgctgcagg aggccctgga gagagacaag gctgccggcc tgattccttt ctctgtggtg 720
 gctacgctgg ggaccacatc gtgctgctcc ttgacaatc tcttagaagt gggacccatc 780
 tgtcacgaag aggacatatg gctgcacgtg gatgctgect acgcaggcag tgccttcac 840
 tgccctgagt tccggcacct gctgaatgga gtggagtttg cagattcatt taactttaat 900
 cccacaaaat ggctcttggt gaattttgac tgctcggcta tgtgggtgaa aaggagaacg 960
 gacctgactg gagccttcaa attggacccc gtgtacttaa agcacagcca ccagggctcg 1020
 gggcttatca cggactacag gcaactggcag ctgccactgg gtcggcgatt ccggtcctcg 1080
 aaaatgtggt ttgttttttag gatgtacgga gtcaaggagc tgcaggccta tatccgcaag 1140
 cacgtgcagc tgtctcatga gtttgaggca tttgtgcttc aggatccacg ctttgaagtc 1200
 tgtgccgaag tcacctggg gctgggtgtg ttccggctga agggctccga cggactgaat 1260
 gaagcgcttc tggaaaggat aaacagcgcc aggaaaatcc acttggttcc ctgtcgctg 1320
 aggggccagt tcgtgctgcg gttcgccatc tgctcgcgca aggtggagtc gggccacgtg 1380
 cggtggcctt gggagcacat ccgagggctg gcggccgagc tgctggccgc ggaggaggga 1440
 aaggcagaga tcaaaagttg a 1461

<210> 54
 <211> 486
 <212> PRT
 <213> Sus scrofa

<400> 54

Met Asn Ala Ser Asp Phe Arg Arg Arg Gly Lys Glu Met Val Asp Tyr
 1 5 10 15

Met Ala Asp Tyr Leu Glu Gly Ile Glu Gly Arg Gln Val Tyr Pro Asp
 20 25 30

Val Gln Pro Gly Tyr Leu Arg Pro Leu Ile Pro Ala Thr Ala Pro Gln
 35 40 45

Glu Pro Asp Thr Phe Glu Asp Ile Leu Gln Asp Val Glu Lys Ile Ile
 50 55 60

Met Pro Gly Val Thr His Trp His Ser Pro Tyr Phe Phe Ala Tyr Phe
 65 70 75 80

Pro Thr Ala Ser Ser Tyr Pro Ala Met Leu Ala Asp Met Leu Cys Gly

85

90

95

Ala Ile Gly Cys Ile Gly Phe Ser Trp Ala Ala Ser Pro Ala Cys Thr
 100 105 110

Glu Leu Glu Thr Val Met Met Asp Trp Leu Gly Lys Met Leu Gln Leu
 115 120 125

Pro Glu Ala Phe Leu Ala Gly Glu Ala Gly Glu Gly Gly Gly Val Ile
 130 135 140

Gln Gly Ser Ala Ser Glu Ala Thr Leu Val Ala Leu Leu Ala Ala Arg
 145 150 155 160

Thr Lys Val Val Arg Arg Leu Gln Ala Ala Ser Pro Gly Leu Thr Gln
 165 170 175

Gly Ala Val Leu Glu Lys Leu Val Ala Tyr Ala Ser Asp Gln Ala His
 180 185 190

Ser Ser Val Glu Arg Ala Gly Leu Ile Gly Gly Val Lys Leu Lys Ala
 195 200 205

Ile Pro Ser Asp Gly Lys Phe Ala Met Arg Ala Ser Ala Leu Gln Glu
 210 215 220

Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Val Val
 225 230 235 240

Ala Thr Leu Gly Thr Thr Ser Cys Cys Ser Phe Asp Asn Leu Leu Glu
 245 250 255

Val Gly Pro Ile Cys His Glu Glu Asp Ile Trp Leu His Val Asp Ala
 260 265 270

Ala Tyr Ala Gly Ser Ala Phe Ile Cys Pro Glu Phe Arg His Leu Leu
 275 280 285

Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys Trp
 290 295 300

Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Arg Arg Thr
 305 310 315 320

Asp Leu Thr Gly Ala Phe Lys Leu Asp Pro Val Tyr Leu Lys His Ser
325 330 335

His Gln Gly Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Leu Pro
340 345 350

Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg Met
355 360 365

Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln Leu
370 375 380

Ser His Glu Phe Glu Ala Phe Val Leu Gln Asp Pro Arg Phe Glu Val
385 390 395 400

Cys Ala Glu Val Thr Leu Gly Leu Val Cys Phe Arg Leu Lys Gly Ser
405 410 415

Asp Gly Leu Asn Glu Ala Leu Leu Glu Arg Ile Asn Ser Ala Arg Lys
420 425 430

Ile His Leu Val Pro Cys Arg Leu Arg Gly Gln Phe Val Leu Arg Phe
435 440 445

Ala Ile Cys Ser Arg Lys Val Glu Ser Gly His Val Arg Leu Ala Trp
450 455 460

Glu His Ile Arg Gly Leu Ala Ala Glu Leu Leu Ala Ala Glu Glu Gly
465 470 475 480

Lys Ala Glu Ile Lys Ser
485

<210> 55
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic gene derived from Sus scrofa L-aromatic amino acid decarboxylase, having numerous codons replaced with others encoding the same amino acids to reduce free energy of folding, and a gly codon inserted after the initiating met codon

<400> 55
atgggtaacg cttccgattt ccgtcgtcgt ggcaaagaaa tggtagacta catggcagat 60
tatctggaag gtatcgaagg ccgtcaagtt taccgggacg ttcagccagg ctatctgcgt 120
ccgctcatcc cagctaccgc accgcaagaa ccggacacct ttgaagacat cctgcaagac 180
gtagaaaaga tcatcatgcc aggtgtaacc cactggcact ctccgtactt tttcgcatac 240
ttcccgactg catcctccta cccggctatg ctggctgaca tgctgtgtgg tgctatcggc 300
tgtatcggct tttcctgggc tgcattctcg gcatgcactg agctggaaac cgttatgatg 360
gattggctgg gtaaaatgct gcagctgcc aaggcatttc tggctggtga ggctggtgag 420
gggtggtggtg taattcaagg ctctgcgtcc gaagctactc tggttgctct gctggctgct 480
cgtactaaag ttgttcgtcg tctgcaagct gcatctccgg gtctgactca ggggtgctgtt 540
ctggagaaac tggtagcgta tgcttctgat caggctcact cttccgttga gcgtgctggt 600
ctgattggtg gtgttaagct gaaagctatt ccgtccgatg gtaagtccgc tatgcgtgca 660
tccgctctgc aagaagctct ggaacgtgac aaagctgctg gtctgattcc gttcttcggt 720
gttgctaccc tgggtactac ctcttgctgt tctttcgaca acctgctgga agttggtccg 780
atctgtcacg aggaggacat ctggctgcac gttgacgcag catatgctgg ctctgctttt 840
atctgtccgg aattccgtca cctgctgaac ggcgttgagt tcgctgattc tttcaacttc 900
aaccgcaca agtggctgct ggttaacttt gattgctcgg ctatgtgggt aaaacgtcgc 960
actgatctga ccggtgcatt taaactggac ccggtatata tgaagcattc tcaccagggt 1020
tccggcctga ttaccgatta tcgtcattgg cagctgccgc tgggtcgtcg ttttcgttcg 1080
ctgaagatgt ggttcgtatt ccgtatgtac ggcgttaaag gtctgcaagc atacatccgt 1140
aaacacgttc aactgtcgca cgagttcgaa gctttcgtac tgcaggaccc gcgttttgaa 1200
gtttgcgctg aagttaccct gggcctgggt tgcttcgctc tgaagggttc tgatggtctg 1260
aacgaagctc tgctggagcg tattaactcg gctcgtaaaa tccacctggt tccgtgtcgt 1320
ctgcgtggtc agttcgttct gcgcttcgct atttgttcgc gtaaggtaga gtctggtcat 1380
gttcgtctgg catgggagca catccgtggt ctggctgctg aactgctggc tgctgaagaa 1440
ggtaaggctg aaatcaaata ctaa 1464

<210> 56
<211> 487
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic protein derived from Sus scrofa L-aromatic amino acid decarboxylase, having a glycine inserted at position 2 in the amino acid sequence

<400> 56

Met Gly Asn Ala Ser Asp Phe Arg Arg Arg Gly Lys Glu Met Val Asp
1 5 10 15

Tyr Met Ala Asp Tyr Leu Glu Gly Ile Glu Gly Arg Gln Val Tyr Pro
20 25 30

Asp Val Gln Pro Gly Tyr Leu Arg Pro Leu Ile Pro Ala Thr Ala Pro
35 40 45

Gln Glu Pro Asp Thr Phe Glu Asp Ile Leu Gln Asp Val Glu Lys Ile
50 55 60

Ile Met Pro Gly Val Thr His Trp His Ser Pro Tyr Phe Phe Ala Tyr
65 70 75 80

Phe Pro Thr Ala Ser Ser Tyr Pro Ala Met Leu Ala Asp Met Leu Cys
85 90 95

Gly Ala Ile Gly Cys Ile Gly Phe Ser Trp Ala Ala Ser Pro Ala Cys
100 105 110

Thr Glu Leu Glu Thr Val Met Met Asp Trp Leu Gly Lys Met Leu Gln
115 120 125

Leu Pro Glu Ala Phe Leu Ala Gly Glu Ala Gly Glu Gly Gly Gly Val
130 135 140

Ile Gln Gly Ser Ala Ser Glu Ala Thr Leu Val Ala Leu Leu Ala Ala
145 150 155 160

Arg Thr Lys Val Val Arg Arg Leu Gln Ala Ala Ser Pro Gly Leu Thr
165 170 175

Gln Gly Ala Val Leu Glu Lys Leu Val Ala Tyr Ala Ser Asp Gln Ala
180 185 190

His Ser Ser Val Glu Arg Ala Gly Leu Ile Gly Gly Val Lys Leu Lys
195 200 205

Ala Ile Pro Ser Asp Gly Lys Phe Ala Met Arg Ala Ser Ala Leu Gln
210 215 220

Glu Ala Leu Glu Arg Asp Lys Ala Ala Gly Leu Ile Pro Phe Phe Val
225 230 235 240

Val Ala Thr Leu Gly Thr Thr Ser Cys Cys Ser Phe Asp Asn Leu Leu
245 250 255

Glu Val Gly Pro Ile Cys His Glu Glu Asp Ile Trp Leu His Val Asp
260 265 270

Ala Ala Tyr Ala Gly Ser Ala Phe Ile Cys Pro Glu Phe Arg His Leu
275 280 285

Leu Asn Gly Val Glu Phe Ala Asp Ser Phe Asn Phe Asn Pro His Lys
290 295 300

Trp Leu Leu Val Asn Phe Asp Cys Ser Ala Met Trp Val Lys Arg Arg
305 310 315 320

Thr Asp Leu Thr Gly Ala Phe Lys Leu Asp Pro Val Tyr Leu Lys His
325 330 335

Ser His Gln Gly Ser Gly Leu Ile Thr Asp Tyr Arg His Trp Gln Leu
340 345 350

Pro Leu Gly Arg Arg Phe Arg Ser Leu Lys Met Trp Phe Val Phe Arg
355 360 365

Met Tyr Gly Val Lys Gly Leu Gln Ala Tyr Ile Arg Lys His Val Gln
370 375 380

Leu Ser His Glu Phe Glu Ala Phe Val Leu Gln Asp Pro Arg Phe Glu
385 390 395 400

Val Cys Ala Glu Val Thr Leu Gly Leu Val Cys Phe Arg Leu Lys Gly
405 410 415

Ser Asp Gly Leu Asn Glu Ala Leu Leu Glu Arg Ile Asn Ser Ala Arg
420 425 430

Lys Ile His Leu Val Pro Cys Arg Leu Arg Gly Gln Phe Val Leu Arg
 435 440 445

Phe Ala Ile Cys Ser Arg Lys Val Glu Ser Gly His Val Arg Leu Ala
 450 455 460

Trp Glu His Ile Arg Gly Leu Ala Ala Glu Leu Leu Ala Ala Glu Glu
 465 470 475 480

Gly Lys Ala Glu Ile Lys Ser
 485

<210> 57
 <211> 1098
 <212> DNA
 <213> Candida boidinii

<400> 57
 atgggtaaga ttgtcttagt tctttatgat gctggtaagc acgctgctga tgaagaaaaa 60
 ttatatgggt gtactgaaaa taaattaggt attgctaatt ggttaaaaga tcaaggcat 120
 gaactaatta ctacttctga taaagaaggt gaaacaagtg aattggataa acatatccca 180
 gatgctgata ttatcatcac cactccttcc catcctgctt atatcactaa ggaaagactt 240
 gacaaggcta agaacttaaa attagtcgtt gtcgctggtg ttggttctga tcacattgat 300
 ttagattata ttaatcaaac aggtaagaaa atctcagtc tggaagttac aggttctaatt 360
 gttgtctctg ttgctgaaca cgttgtcatg accatgcttg tcttggttag aaatttcgtt 420
 ccagcacatg aacaaattat taaccacgat tgggaggttg ctgctatcgc taaggatgct 480
 tacgatatcg aaggtaaaac tatcgctacc attggtgctg gtagaattgg ttacagagtc 540
 ttggaaagat tactccatt taatccaaaa gaattattat actacgatta tcaagcttta 600
 ccaaaagaag ctgaagaaaa agttggtgct agaagagttg aaaatattga agaattagtt 660
 gctcaagctg atatcgttac agttaatgct ccattacacg caggtaaaa aggtttaatt 720
 aataaggaat tattatctaa atttaaaaaa ggtgcttggt tagtcaatac cgcaagaggt 780
 gctatttctg ttgctgaaga tggtgcagca gctttagaat ctggtcaatt aagaggttac 840
 ggtggtgatg tttggttccc acaaccagct ccaaaggatc acccatggag agatatgaga 900
 aataaatatg gtgctggtaa tgccatgact cctcactact ctggtactac tttagacgct 960
 caaacaagat acgctgaagg tactaaaaat attttggaaat cattctttac cggtaaattt 1020

gattacagac cacaagatat tatcttatta aatgggtgaat acgttactaa agcttacggt 1080

aaacacgata agaaataa 1098

<210> 58
<211> 365
<212> PRT
<213> Candida boidinii

<400> 58

Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala
1 5 10 15

Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala
20 25 30

Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys
35 40 45

Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile
50 55 60

Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu
65 70 75 80

Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser
85 90 95

Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser
100 105 110

Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val
115 120 125

Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu
130 135 140

Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala
145 150 155 160

Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile
165 170 175

Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu

180

185

190

Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val
 195 200 205

Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp
 210 215 220

Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile
 225 230 235 240

Asn Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn
 245 250 255

Thr Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu
 260 265 270

Glu Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln
 275 280 285

Pro Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly
 290 295 300

Ala Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala
 305 310 315 320

Gln Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe
 325 330 335

Thr Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly
 340 345 350

Glu Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
 355 360 365

<210> 59
 <211> 1098
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic gene derived from Candida boidinii formate dehydrogenase, having numerous codons replaced with others encoding the same amino acids to reduce free energy of folding, and a gly codon inserted after the initiating met codon to insert a restriction site

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<400> 59
atgggcaaaa tcgttctggt tctgtatgac gctggtaaac acgctgctga cgaagaaaaa 60
ctgtacggct gcaccgaaaa caaactgggt atcgctaact ggctgaaaga tcagggtcac 120
gaactgatca ctacctctga caaagaaggt gaaacctctg aactggacaa acacatcccg 180
gatgcagata tcatcatcac cactccgttc caccggctt acatcaccaa agagcgtctg 240
gacaaagcta aaaacctgaa actggtagta gttgctggtg taggttctga ccacatcgac 300
ctggactaca tcaaccagac tggtaaaaaa atctctgtac tggaagtaac tggttctaac 360
gttgtttctg ttgctgaaca cgttgtaatg actatgctgg ttctgggtcg taacttcggt 420
ccggctcacg aacagatcat caaccacgat tgggaagttg cagcaatcgc taaagacgct 480
tatgacatcg aaggcaaaac catcgctact atcggcgctg gccgtatcgg ttaccgtggt 540
ctggaacgct tgctgccgtt caaccgaaa gaactgctgt actacgacta ccaggctctg 600
ccgaaagaag cagaggagaa agttggtgct cgccgtgtag agaacatcga agagctggta 660
gctcaggctg acatcgttac tgtaaacgct ccgctgcacg caggcactaa aggtctgatt 720
aaciaagagc tgctgtctaa attcaaaaaa ggtgcatggc tggtaaacac tgcacgtggt 780
gctatctgcg ttgctgaaga cgttgctgct gcactggaat ctggtcagct gcgtgggttac 840
ggtggtgacg tatggtttcc gcagccggct ccgaaagatc acccgtggcg tgatatgcgt 900
aaciaatatg gcgctggtaa cgcaatgacc ccgcactact ctggtaccac tctggatgct 960
cagaccggtt acgctgaagg tactaaaaac atcctggaat ctttcttcac tggtaaattc 1020
gactaccgcc cgcaggacat cattctgctg aacggtgaat atgtaactaa agcttacggc 1080
aaacacgaca aaaaataa 1098

```

```

<210> 60
<211> 365
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Synthetic protein derived from Candida boidinii formate dehydroge
nase, having a glycine inserted after the initiating methionine

```

```

<400> 60
Met Gly Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala
1           5           10           15

```

```

Asp Glu Glu Lys Leu Tyr Gly Cys Thr Glu Asn Lys Leu Gly Ile Ala

```

20

25

30

Asn Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys
 35 40 45

Glu Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile
 50 55 60

Ile Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu
 65 70 75 80

Asp Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser
 85 90 95

Asp His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser
 100 105 110

Val Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val
 115 120 125

Val Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu
 130 135 140

Gln Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala
 145 150 155 160

Tyr Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile
 165 170 175

Gly Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu
 180 185 190

Leu Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val
 195 200 205

Gly Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp
 210 215 220

Ile Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile
 225 230 235 240

Asn Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn
 245 250 255

Thr Ala Arg Gly Ala Ile Cys Val Ala Glu Asp Val Ala Ala Ala Leu
 260 265 270

Glu Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln
 275 280 285

Pro Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly
 290 295 300

Ala Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala
 305 310 315 320

Gln Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe
 325 330 335

Thr Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly
 340 345 350

Glu Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
 355 360 365

<210> 61
 <211> 1488
 <212> DNA
 <213> Pseudomonas putida

<400> 61
 atgtccctgt tgatccgtgg cgccaccgtg gtcacccacg aagagagtta ccccgccgat 60
 gtccctgtgtg tcgatggcct gatccgtgcc atcgggccaa acctcgaacc gccaccgac 120
 tgtgaaatcc tcgacggcag cggccagtac ctgatgcccg gcggcatcga cccgcatacc 180
 cacatgcagt tgccattcat gggcaccgtg gccagcgagg atttcttcag cggcaccgca 240
 gcggggccttg ccggcggcac cacgtcgatc atcgacttcg tcatcccca cccgcagcag 300
 tcattgctgg aggccttcca cacctggcgc ggcctgggcgc agaagagcgc cagcgactac 360
 ggcttccacg ttgccatcac ctggtggagc gaacaggtgg ctgaagaaat gggcgaactg 420
 gtagccaagc atggggtgaa cagcttcaag cacttcatgg cttacaagaa tgcaatcatg 480
 gccgccgacg acaccctggt ggccagcttc gagcgctgcc tgcaactggg tgccgtgccc 540
 accgtgcatg ccgagaacgg cgaactggtg taccacctgc agaaaaaact gcttgcccag 600
 ggcattgaccg gaccagagcg tcacccctt tcgcgcctt cacaagtgga aggtgaagcg 660

gccagccgcg ccatccgtat tgccgaaacc attggtacgc cgctgtatgt ggtgcacatt 720
 tccagccgtg aagcactgga tgaaatcacc tatgcacgcg ccaagggcca gccgggtttac 780
 ggcgaagtct tgcccggcca cctgctgctg gacgacagcg tctaccgtga cccggactgg 840
 gccactgccg ctggctacgt gatgagcccg ccgttccgcc cgcgcgagca ccaggaggcg 900
 ctgtggcgcg gcttgcagtc gggcaacctg cacaccacgg ccaccgacca ctgctgtttc 960
 tgcgccgaac agaaagccat gggccgcgac gacttcagtc gcatcccca cggcaccgcc 1020
 ggcacgaag accgcatggc ggtgctgtgg gatgccggtg tcaacagcgg gcgcctgtcg 1080
 atgcatgagt tcgttgcgct gacctccacc aacacggcaa aaatcttcaa ccttttccca 1140
 cgcaagggcg ccatccgcgt gggtgccgac gccgacctgg tgctgtggga cccgcagggc 1200
 actgcactc tatcggccca gaccaccac cagcgggtgg acttcaatat ctttgaaggc 1260
 cgcactgtgc gcgggggtccc cagccacacc atcagccagg gcaaggtgct ctgggccgat 1320
 ggcgacctgc gtcgccgagg ccggggcggg gcggtatgtg gaacggccgg cgtatccgtc 1380
 ggtgtacgag gtgctggggc gacgcgccga acagcagcgc ccgacgcccg ttcagcgctg 1440
 aggccattgg ggctgctgcg cagcccatcg ccggcaagcc aaatataa 1488

<210> 62
 <211> 495
 <212> PRT
 <213> *Pseudomonas putida*

<400> 62

Met Ser Leu Leu Ile Arg Gly Ala Thr Val Val Thr His Glu Glu Ser
 1 5 10 15

Tyr Pro Ala Asp Val Leu Cys Val Asp Gly Leu Ile Arg Ala Ile Gly
 20 25 30

Pro Asn Leu Glu Pro Pro Thr Asp Cys Glu Ile Leu Asp Gly Ser Gly
 35 40 45

Gln Tyr Leu Met Pro Gly Gly Ile Asp Pro His Thr His Met Gln Leu
 50 55 60

Pro Phe Met Gly Thr Val Ala Ser Glu Asp Phe Phe Ser Gly Thr Ala
 65 70 75 80

Ala Gly Leu Ala Gly Gly Thr Thr Ser Ile Ile Asp Phe Val Ile Pro
85 90 95

Asn Pro Gln Gln Ser Leu Leu Glu Ala Phe His Thr Trp Arg Gly Trp
100 105 110

Ala Gln Lys Ser Ala Ser Asp Tyr Gly Phe His Val Ala Ile Thr Trp
115 120 125

Trp Ser Glu Gln Val Ala Glu Glu Met Gly Glu Leu Val Ala Lys His
130 135 140

Gly Val Asn Ser Phe Lys His Phe Met Ala Tyr Lys Asn Ala Ile Met
145 150 155 160

Ala Ala Asp Asp Thr Leu Val Ala Ser Phe Glu Arg Cys Leu Gln Leu
165 170 175

Gly Ala Val Pro Thr Val His Ala Glu Asn Gly Glu Leu Val Tyr His
180 185 190

Leu Gln Lys Lys Leu Leu Ala Gln Gly Met Thr Gly Pro Glu Ala His
195 200 205

Pro Leu Ser Arg Pro Ser Gln Val Glu Gly Glu Ala Ala Ser Arg Ala
210 215 220

Ile Arg Ile Ala Glu Thr Ile Gly Thr Pro Leu Tyr Val Val His Ile
225 230 235 240

Ser Ser Arg Glu Ala Leu Asp Glu Ile Thr Tyr Ala Arg Ala Lys Gly
245 250 255

Gln Pro Val Tyr Gly Glu Val Leu Pro Gly His Leu Leu Leu Asp Asp
260 265 270

Ser Val Tyr Arg Asp Pro Asp Trp Ala Thr Ala Ala Gly Tyr Val Met
275 280 285

Ser Pro Pro Phe Arg Pro Arg Glu His Gln Glu Ala Leu Trp Arg Gly
290 295 300

Leu Gln Ser Gly Asn Leu His Thr Thr Ala Thr Asp His Cys Cys Phe

305 310 315 320
 Cys Ala Glu Gln Lys Ala Met Gly Arg Asp Asp Phe Ser Arg Ile Pro
 325 330 335
 Asn Gly Thr Ala Gly Ile Glu Asp Arg Met Ala Val Leu Trp Asp Ala
 340 345 350
 Gly Val Asn Ser Gly Arg Leu Ser Met His Glu Phe Val Ala Leu Thr
 355 360 365
 Ser Thr Asn Thr Ala Lys Ile Phe Asn Leu Phe Pro Arg Lys Gly Ala
 370 375 380
 Ile Arg Val Gly Ala Asp Ala Asp Leu Val Leu Trp Asp Pro Gln Gly
 385 390 395 400
 Thr Arg Thr Leu Ser Ala Gln Thr His His Gln Arg Val Asp Phe Asn
 405 410 415
 Ile Phe Glu Gly Arg Thr Val Arg Gly Val Pro Ser His Thr Ile Ser
 420 425 430
 Gln Gly Lys Val Leu Trp Ala Asp Gly Asp Leu Arg Arg Arg Gly Arg
 435 440 445
 Gly Gly Ala Val Cys Gly Thr Ala Gly Val Ser Val Gly Val Arg Gly
 450 455 460
 Ala Gly Ala Thr Arg Arg Thr Ala Ala Pro Asp Ala Arg Ser Ala Leu
 465 470 475 480
 Arg Pro Leu Gly Leu Leu Arg Ser Pro Ser Pro Ala Ser Gln Ile
 485 490 495

<210> 63
 <211> 1491
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic gene derived from Pseudomonas putida hydantoinase, having numerous codons replaced with others encoding the same amino acids to reduce free energy of folding, and a gly codon inserted after the initiating met codon to insert a restriction site

<400> 63

atgggctctc tgctgatccg tgggtgctacc gttgtttaccc acgaagaatc ttatccggct	60
gacgttctgt gcgttgacgg tctgatccgt gctatcggtc cgaacctgga accgccgacc	120
gactgcgaaa tcctggacgg ttctggtcag tacctgatgc cgggtgggtat cgacccgcat	180
actcacatgc agctgccgtt tatgggtact gttgcttctg aagacttctt ctctggcacc	240
gctgctggtc tggctgggtg taccacctct atcatcgact tcgttatccc gaacccgcag	300
cagtctctgc tggaagcttt ccatacttgg cgtgggtggg ctcagaaatc tgcattctgac	360
tacggtttcc acgttgctat cacctgggtg tctgaacagg ttgctgaaga aatgggcgaa	420
ctggttgcta aacacgggtg taactcttcc aaacacttca tggcttaca aaacgcaatt	480
atggcggctg acgacactct ggttgcttct ttcgaacgct gtctgcagct gggcgctgtt	540
ccgaccgttc acgctgaaaa cggcgagctg gtttatcacc tgcagaaaaa actgctggct	600
cagggatga ctggcccgga agctcaccgc ctgtctcgtc cgtctcaggt tgagggcgaa	660
gctgcttctc gtgctatccg tatcgctgaa accatcggtc ccccgctgta tgtagttcat	720
atctcttctc gtgaagctct ggatgagatt acttacgcac gtgctaaggg tcagccgggt	780
tacggatgaag ttctgccggg tcatctgctg ctggatgatt ctgtataccg cgatccggac	840
tgggcaactg ctgctgggtt cgttatgtcc ccgccgttcc gtccgcgtga gcatcaggag	900
gcactgtggc gcggcctgca gtctggtaac ctgcatacta ctgctactga tcaactgttgt	960
ttctgcgctg agcagaaggc tatgggtcgc gatgacttct ctgcattcc gaacggtact	1020
gctggcattg aggaccgtat ggctgttctg tgggatgctg gcgttaactc tggctgctctg	1080
tctatgcacg aattcgttgc tctgacctct actaacactg ctaaaatctt caacctgttc	1140
ccgcgtaaag gtgcaatccg cgtaggtgca gatgctgac tggttctgtg ggatccgcag	1200
ggcactcgca ctctgtctgc tcagactcat catcagcgtg ttgacttcaa catctttgag	1260
ggccgtactg ttcgcgggtg tccgtctcat accatctctc agggtaaagt tctgtgggct	1320
gacggtgacc tgcgtcgtcg tggctggtg ggtgctgttt gcggtaccgc tgggtgttct	1380
gttgggtgtc gtggcgctgg tgctaccgt cgtactgctg ctccggatgc tcgttctgct	1440
ctgcgtccgc tgggtctgct gcgttctccg tctccggctt ctcagattta a	1491

<210> 64
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Synthetic protein derived from Pseudomonas putida hydantoinase, having a glycine residue inserted after the initiating methionine

<400> 64

Met Gly Ser Leu Leu Ile Arg Gly Ala Thr Val Val Thr His Glu Glu
1 5 10 15

Ser Tyr Pro Ala Asp Val Leu Cys Val Asp Gly Leu Ile Arg Ala Ile
20 25 30

Gly Pro Asn Leu Glu Pro Pro Thr Asp Cys Glu Ile Leu Asp Gly Ser
35 40 45

Gly Gln Tyr Leu Met Pro Gly Gly Ile Asp Pro His Thr His Met Gln
50 55 60

Leu Pro Phe Met Gly Thr Val Ala Ser Glu Asp Phe Phe Ser Gly Thr
65 70 75 80

Ala Ala Gly Leu Ala Gly Gly Thr Thr Ser Ile Ile Asp Phe Val Ile
85 90 95

Pro Asn Pro Gln Gln Ser Leu Leu Glu Ala Phe His Thr Trp Arg Gly
100 105 110

Trp Ala Gln Lys Ser Ala Ser Asp Tyr Gly Phe His Val Ala Ile Thr
115 120 125

Trp Trp Ser Glu Gln Val Ala Glu Glu Met Gly Glu Leu Val Ala Lys
130 135 140

His Gly Val Asn Ser Phe Lys His Phe Met Ala Tyr Lys Asn Ala Ile
145 150 155 160

Met Ala Ala Asp Asp Thr Leu Val Ala Ser Phe Glu Arg Cys Leu Gln
165 170 175

Leu Gly Ala Val Pro Thr Val His Ala Glu Asn Gly Glu Leu Val Tyr
180 185 190

His Leu Gln Lys Lys Leu Leu Ala Gln Gly Met Thr Gly Pro Glu Ala
195 200 205

His Pro Leu Ser Arg Pro Ser Gln Val Glu Gly Glu Ala Ala Ser Arg
210 215 220

Ala Ile Arg Ile Ala Glu Thr Ile Gly Thr Pro Leu Tyr Val Val His
225 230 235 240

Ile Ser Ser Arg Glu Ala Leu Asp Glu Ile Thr Tyr Ala Arg Ala Lys
245 250 255

Gly Gln Pro Val Tyr Gly Glu Val Leu Pro Gly His Leu Leu Leu Asp
260 265 270

Asp Ser Val Tyr Arg Asp Pro Asp Trp Ala Thr Ala Ala Gly Tyr Val
275 280 285

Met Ser Pro Pro Phe Arg Pro Arg Glu His Gln Glu Ala Leu Trp Arg
290 295 300

Gly Leu Gln Ser Gly Asn Leu His Thr Thr Ala Thr Asp His Cys Cys
305 310 315 320

Phe Cys Ala Glu Gln Lys Ala Met Gly Arg Asp Asp Phe Ser Arg Ile
325 330 335

Pro Asn Gly Thr Ala Gly Ile Glu Asp Arg Met Ala Val Leu Trp Asp
340 345 350

Ala Gly Val Asn Ser Gly Arg Leu Ser Met His Glu Phe Val Ala Leu
355 360 365

Thr Ser Thr Asn Thr Ala Lys Ile Phe Asn Leu Phe Pro Arg Lys Gly
370 375 380

Ala Ile Arg Val Gly Ala Asp Ala Asp Leu Val Leu Trp Asp Pro Gln
385 390 395 400

Gly Thr Arg Thr Leu Ser Ala Gln Thr His His Gln Arg Val Asp Phe
405 410 415

Asn Ile Phe Glu Gly Arg Thr Val Arg Gly Val Pro Ser His Thr Ile
420 425 430

Ser Gln Gly Lys Val Leu Trp Ala Asp Gly Asp Leu Arg Arg Arg Gly
 435 440 445

Arg Gly Gly Ala Val Cys Gly Thr Ala Gly Val Ser Val Gly Val Arg
 450 455 460

Gly Ala Gly Ala Thr Arg Arg Thr Ala Ala Pro Asp Ala Arg Ser Ala
 465 470 475 480

Leu Arg Pro Leu Gly Leu Leu Arg Ser Pro Ser Pro Ala Ser Gln Ile
 485 490 495

<210> 65
 <211> 1683
 <212> DNA
 <213> Penicillium simplicissimum

<400> 65
 atgtccaaga cacaggaatt caggcctttg acactgccac ccaagctgtc gttaagtgc 60
 ttcaatgaat tcatccagga tattattcga atcgttggct ctgaaaatgt tgaagtcatt 120
 agctcgaagg accagattgt tgacggttct tatatgaaac ctacgcacac gcacgatccc 180
 catcatgtca tggaccagga ctacttcctt gcctcagcaa ttgttgctcc tcgcaatgtc 240
 gccgatgtgc agtcgattgt cggacttgcc aataagttct catttccct ctggcccatc 300
 tctattggaa gaaattccgg atatggcggt gctgcgccac gggtagtg cagtgtcgtg 360
 ctggacatgg gaaagaatat gaacagagtt ctagaagtga acgtggaagg cgcattatgc 420
 gtggtggagc cgggtgtaac ttaccacgac ttgcataatt accttgaggc gaacaatctt 480
 cgagacaaat tatggcttga tgtaccggat cttggtggcg gttctgttct cggcaatgcc 540
 gttgagagag gtgtgggcta tacgccttac ggagatcatt ggatgatgca cagtgggatg 600
 gaagtcgtcc ttgcgaatgg cgagcttctt aggactggca tgggggctct acctgatcct 660
 aaacgtcccg aaacgatggg gctaaagcca gaagaccagc catggagcaa aatcgtcat 720
 ctgtttcctt atggettcgg tccctatata gatgggctat tcagccaatc gaatatggga 780
 attgttacca agatcgggat ctggttaatg cccaatccag ggggttatca atcctacttg 840
 atcacactac ccaaagatgg tgatttaaaa caagccgtcg atattattcg tccccttcgt 900
 ctaggcattg cccttcaaaa tgttcccact attcgccaca ttcttttgga tgcagcggtg 960
 ctcggtgaca agcgatctta tcatccaag accgaacccc tctccgacga ggaattagac 1020

aagatcgga aacagctcaa cttgggacga tggaaactttt acggggcgct ctatggacct 1080
gagccgattc gaagggttct ctgggaaacg attaaagacg cattctcggc gatcccaggc 1140
gtcaagtttt attttccgga ggacactcct gaaaactccg ttctccgcgt gcgtgataag 1200
actatgcaag gcattccaac ttacgacgag ctaaagtgga tcgattggct ccctaattggt 1260
gcgcattctgt tcttctctcc tattgcaag gtatctggtg aagatgcaat gatgcaatac 1320
gcagtcacca agaaaagggtg tcaggaggct gggttagatt ttatcggcac ttccacagtc 1380
ggatgagag agatgcatca tatcgtttgt attgtgttca acaagaagga cctaatacaa 1440
aagagaaaag tacagtggct gatgagaacc cttattgatg actgtgctgc aaatggatgg 1500
ggcgaatata gaacccatct ggccttcatt gaccaaatta tggaaaccta caactggaac 1560
aacagcagct tcctaagggt caatgaggct ctcaagaatg cggatggatcc taatggcatc 1620
attgccccgg gaaagtctgg tgtttggccg agtcaataca gtcattgttac ttggaaactg 1680
taa 1683

<210> 66
<211> 560
<212> PRT
<213> *Penicillium simplicissimum*

<400> 66

Met Ser Lys Thr Gln Glu Phe Arg Pro Leu Thr Leu Pro Pro Lys Leu
1 5 10 15

Ser Leu Ser Asp Phe Asn Glu Phe Ile Gln Asp Ile Ile Arg Ile Val
20 25 30

Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val Asp
35 40 45

Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val Met
50 55 60

Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn Val
65 70 75 80

Ala Asp Val Gln Ser Ile Val Gly Leu Ala Asn Lys Phe Ser Phe Pro
85 90 95

Leu Trp Pro Ile Ser Ile Gly Arg Asn Ser Gly Tyr Gly Gly Ala Ala

100

105

110

Pro Arg Val Ser Gly Ser Val Val Leu Asp Met Gly Lys Asn Met Asn
 115 120 125

Arg Val Leu Glu Val Asn Val Glu Gly Ala Tyr Cys Val Val Glu Pro
 130 135 140

Gly Val Thr Tyr His Asp Leu His Asn Tyr Leu Glu Ala Asn Asn Leu
 145 150 155 160

Arg Asp Lys Leu Trp Leu Asp Val Pro Asp Leu Gly Gly Gly Ser Val
 165 170 175

Leu Gly Asn Ala Val Glu Arg Gly Val Gly Tyr Thr Pro Tyr Gly Asp
 180 185 190

His Trp Met Met His Ser Gly Met Glu Val Val Leu Ala Asn Gly Glu
 195 200 205

Leu Leu Arg Thr Gly Met Gly Ala Leu Pro Asp Pro Lys Arg Pro Glu
 210 215 220

Thr Met Gly Leu Lys Pro Glu Asp Gln Pro Trp Ser Lys Ile Ala His
 225 230 235 240

Leu Phe Pro Tyr Gly Phe Gly Pro Tyr Ile Asp Gly Leu Phe Ser Gln
 245 250 255

Ser Asn Met Gly Ile Val Thr Lys Ile Gly Ile Trp Leu Met Pro Asn
 260 265 270

Pro Gly Gly Tyr Gln Ser Tyr Leu Ile Thr Leu Pro Lys Asp Gly Asp
 275 280 285

Leu Lys Gln Ala Val Asp Ile Ile Arg Pro Leu Arg Leu Gly Met Ala
 290 295 300

Leu Gln Asn Val Pro Thr Ile Arg His Ile Leu Leu Asp Ala Ala Val
 305 310 315 320

Leu Gly Asp Lys Arg Ser Tyr Ser Ser Lys Thr Glu Pro Leu Ser Asp
 325 330 335

Glu Glu Leu Asp Lys Ile Ala Lys Gln Leu Asn Leu Gly Arg Trp Asn
340 345 350

Phe Tyr Gly Ala Leu Tyr Gly Pro Glu Pro Ile Arg Arg Val Leu Trp
355 360 365

Glu Thr Ile Lys Asp Ala Phe Ser Ala Ile Pro Gly Val Lys Phe Tyr
370 375 380

Phe Pro Glu Asp Thr Pro Glu Asn Ser Val Leu Arg Val Arg Asp Lys
385 390 395 400

Thr Met Gln Gly Ile Pro Thr Tyr Asp Glu Leu Lys Trp Ile Asp Trp
405 410 415

Leu Pro Asn Gly Ala His Leu Phe Phe Ser Pro Ile Ala Lys Val Ser
420 425 430

Gly Glu Asp Ala Met Met Gln Tyr Ala Val Thr Lys Lys Arg Cys Gln
435 440 445

Glu Ala Gly Leu Asp Phe Ile Gly Thr Phe Thr Val Gly Met Arg Glu
450 455 460

Met His His Ile Val Cys Ile Val Phe Asn Lys Lys Asp Leu Ile Gln
465 470 475 480

Lys Arg Lys Val Gln Trp Leu Met Arg Thr Leu Ile Asp Asp Cys Ala
485 490 495

Ala Asn Gly Trp Gly Glu Tyr Arg Thr His Leu Ala Phe Met Asp Gln
500 505 510

Ile Met Glu Thr Tyr Asn Trp Asn Asn Ser Ser Phe Leu Arg Phe Asn
515 520 525

Glu Val Leu Lys Asn Ala Val Asp Pro Asn Gly Ile Ile Ala Pro Gly
530 535 540

Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys Leu
545 550 555 560

<210> 67
<211> 1686
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic gene derived from *Penicillium simplicissimum* vanillyl alcohol oxidase, having numerous codons replaced with others encoding the same amino acids to reduce free energy of folding and a gly codon inserted after the initiating met codon to insert a restriction site

<400> 67

```
atgggctcta aaactcagga gttccgtccg ctgaccctgc cgccgaaact gtctctgtct      60
gattttaacg aattcatcca ggatatcatc cgtatcgttg gttctgaaaa cgttgaagtt      120
atctcttcta aagaccagat cgttgacggt tcttacatga aaccgaccca caccacgac      180
ccgcaccacg ttatggacca ggactacttc ctggcttctg ctatcgttgc tccgcgtaac      240
gttgctgacg ttcagtctat cgttggtctg gctaacaaat tctctttccc gctgtggccg      300
atctctatcg gtcgtaactc tggttacggt ggtgctgctc cgcgtgtttc tggttctggt      360
gttctggaca tgggtaaaaa catgaaccgt gttctggaag ttaacgttga aggtgcttac      420
tgcgttggtg aaccgggtgt aacttatcat gacctgcaca actacctgga agctaacaac      480
ctgcgtgaca aactgtggct ggacgtaccg gatctgggtg gtggttctgt tctgggtaac      540
gctgttgaac gtggtgttgg ttacaccccg tacggtgatc attggatgat gcactctggc      600
atggaggtag tactggctaa cgggtgaactg ctgcgtaccg gtatgggtgc tctgccggac      660
ccgaagcgtc cggaactat gggctctgaag ccggaggatc agccgtggtc taaaatcgct      720
catctgttcc cgtatggctt tggtcgtac atcgacggtc tgttctctca gtctaacaatg      780
ggtatcgtta ccaaaattgg catttggtctg atgccgaacc cgggtgggta ccagtcttac      840
ctgattactc tgccgaaaga tggcgacctg aaacaggctg ttgatatcat tcgcccgtcg      900
cgtctgggta tggctctgca gaacgttccg actatccgcc acatcctgct ggacgctgca      960
gtactgggtg acaaacgttc ctactcctct aaaactgaac cgctgtctga cgaagaactg     1020
gacaaaatcg ctaaacagct gaacctgggt cgttggaact tctacggtgc tctgtacggt     1080
ccggaaccga tccgtcgtgt tctgtgggag actatcaagg atgctttctc tgctatcccg     1140
gggtgttaaat tctacttccc ggaagacact ccggaaaact ctgttctgcg tgtacgtgac     1200
aaaaccatgc agggtatccc gacctacgac gaactgaaat ggatcgactg gctgccgaac     1260
gggtgctcacc tgttcttttc tccgatcgt aaagtatccg gagaggacgc tatgatgcag     1320
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tatgctgtta ccaaaaaacg ttgtcaggaa gctgggtctgg atttcattgg taccttcact 1380
 gtaggtatgc gcgaaatgca tcatattggt tgcacggttt tcaacaaaaa agacctgatt 1440
 cagaagcgca aagttcagtg gctgatgcgt accctgatcg acgactgtgc tgctaacggt 1500
 tgggggtgaat accgtacca cctggcattc atggaccaga tcatggaaac ctacaactgg 1560
 aacaactctt ctttctcgcg tttcaacgaa gttctgaaaa acgctgttga cccgaacggt 1620
 atcatcgctc cgggtaaatc tgggtgttgg ccgtctcagt actctcacgt tacctggaaa 1680
 ctgtaa 1686

<210> 68
 <211> 561
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic protein derived from Penicillium simplicissium vanillyl
 alcohol oxidase, having a glycine residue inserted after the ini
 tiating methionine

<400> 68

Met Gly Ser Lys Thr Gln Glu Phe Arg Pro Leu Thr Leu Pro Pro Lys
 1 5 10 15

Leu Ser Leu Ser Asp Phe Asn Glu Phe Ile Gln Asp Ile Ile Arg Ile
 20 25 30

Val Gly Ser Glu Asn Val Glu Val Ile Ser Ser Lys Asp Gln Ile Val
 35 40 45

Asp Gly Ser Tyr Met Lys Pro Thr His Thr His Asp Pro His His Val
 50 55 60

Met Asp Gln Asp Tyr Phe Leu Ala Ser Ala Ile Val Ala Pro Arg Asn
 65 70 75 80

Val Ala Asp Val Gln Ser Ile Val Gly Leu Ala Asn Lys Phe Ser Phe
 85 90 95

Pro Leu Trp Pro Ile Ser Ile Gly Arg Asn Ser Gly Tyr Gly Gly Ala
 100 105 110

Ala Pro Arg Val Ser Gly Ser Val Val Leu Asp Met Gly Lys Asn Met

115	120	125
Asn Arg Val Leu Glu Val	Asn Val Glu Gly Ala	Tyr Cys Val Val Glu
130	135	140
Pro Gly Val Thr Tyr His	Asp Leu His Asn Tyr	Leu Glu Ala Asn Asn
145	150	155 160
Leu Arg Asp Lys Leu Trp	Leu Asp Val Pro Asp	Leu Gly Gly Gly Ser
165	170	175
Val Leu Gly Asn Ala Val	Glu Arg Gly Val Gly	Tyr Thr Pro Tyr Gly
180	185	190
Asp His Trp Met Met His	Ser Gly Met Glu Val	Val Leu Ala Asn Gly
195	200	205
Glu Leu Leu Arg Thr Gly	Met Gly Ala Leu Pro	Asp Pro Lys Arg Pro
210	215	220
Glu Thr Met Gly Leu Lys	Pro Glu Asp Gln Pro	Trp Ser Lys Ile Ala
225	230	235 240
His Leu Phe Pro Tyr Gly	Phe Gly Pro Tyr Ile	Asp Gly Leu Phe Ser
245	250	255
Gln Ser Asn Met Gly Ile	Val Thr Lys Ile Gly	Ile Trp Leu Met Pro
260	265	270
Asn Pro Gly Gly Tyr Gln	Ser Tyr Leu Ile Thr	Leu Pro Lys Asp Gly
275	280	285
Asp Leu Lys Gln Ala Val	Asp Ile Ile Arg Pro	Leu Arg Leu Gly Met
290	295	300
Ala Leu Gln Asn Val Pro	Thr Ile Arg His Ile	Leu Leu Asp Ala Ala
305	310	315 320
Val Leu Gly Asp Lys Arg	Ser Tyr Ser Ser Lys	Thr Glu Pro Leu Ser
325	330	335
Asp Glu Glu Leu Asp Lys	Ile Ala Lys Gln Leu	Asn Leu Gly Arg Trp
340	345	350

Asn Phe Tyr Gly Ala Leu Tyr Gly Pro Glu Pro Ile Arg Arg Val Leu
355 360 365

Trp Glu Thr Ile Lys Asp Ala Phe Ser Ala Ile Pro Gly Val Lys Phe
370 375 380

Tyr Phe Pro Glu Asp Thr Pro Glu Asn Ser Val Leu Arg Val Arg Asp
385 390 395 400

Lys Thr Met Gln Gly Ile Pro Thr Tyr Asp Glu Leu Lys Trp Ile Asp
405 410 415

Trp Leu Pro Asn Gly Ala His Leu Phe Phe Ser Pro Ile Ala Lys Val
420 425 430

Ser Gly Glu Asp Ala Met Met Gln Tyr Ala Val Thr Lys Lys Arg Cys
435 440 445

Gln Glu Ala Gly Leu Asp Phe Ile Gly Thr Phe Thr Val Gly Met Arg
450 455 460

Glu Met His His Ile Val Cys Ile Val Phe Asn Lys Lys Asp Leu Ile
465 470 475 480

Gln Lys Arg Lys Val Gln Trp Leu Met Arg Thr Leu Ile Asp Asp Cys
485 490 495

Ala Ala Asn Gly Trp Gly Glu Tyr Arg Thr His Leu Ala Phe Met Asp
500 505 510

Gln Ile Met Glu Thr Tyr Asn Trp Asn Asn Ser Ser Phe Leu Arg Phe
515 520 525

Asn Glu Val Leu Lys Asn Ala Val Asp Pro Asn Gly Ile Ile Ala Pro
530 535 540

Gly Lys Ser Gly Val Trp Pro Ser Gln Tyr Ser His Val Thr Trp Lys
545 550 555 560

Leu

<210> 69
 <211> 852
 <212> DNA
 <213> Candida magnoliae

<400> 69
 atggctaaga acttctccaa cgctcgagtac cccgccccgc ctccggccca caccaagaac 60
 gagtcgctgc aggtccttga cctgttcaag ctgaatggca aggttgccag catcactggc 120
 tcgtccagcg gtattggcta cgctctggct gaggccttcg cgcaggctcg cgctgacgtc 180
 gccatctggt acaacagcca cgacgtact ggcaaggctg aggccttcgc caagaagtac 240
 ggcgtcaagg tcaaggccta caaggcgaac gtgagcagct ctgacgccgt gaagcagacg 300
 atcgagcagc agatcaagga cttcggccac ctcgacattg tcgtggcgaa cgccggcatt 360
 ccctggacga aggggtgcta catcgaccag gacgacgaca agcacttcga ccaggctcgtt 420
 gacgtcgatc tgaaggggtg tggatacgtc gcgaagcacg ctggccgtca cttccgcgag 480
 cgcttcgaga aggagggcaa gaaggcgcc cttgtgttca cggcctccat gtctggccac 540
 attgtgaacg tgccccagtt ccaggccacg tacaacgcgg ccaaggctgg cgtgcgccac 600
 ttcgcgaagt cgctggccgt cgagttcgcg ccgttcgcgc gcgtgaactc tgtgtcgccg 660
 ggctacatca acacggagat ctcggaactc gtgccccagg agacgcagaa caagtgggtg 720
 tcgctcgtgc cccttggccg cggcggagag acggccgagc tcgttggcgc ctacctgttc 780
 cttgcatctg acgccggctc gtacgccact ggtacggaca tcattgttga cggtggttac 840
 acgcttcct aa 852

<210> 70
 <211> 283
 <212> PRT
 <213> Candida magnoliae

<400> 70

Met Ala Lys Asn Phe Ser Asn Val Glu Tyr Pro Ala Pro Pro Pro Ala
 1 5 10 15

His Thr Lys Asn Glu Ser Leu Gln Val Leu Asp Leu Phe Lys Leu Asn
 20 25 30

Gly Lys Val Ala Ser Ile Thr Gly Ser Ser Ser Gly Ile Gly Tyr Ala
 35 40 45

Leu Ala Glu Ala Phe Ala Gln Val Gly Ala Asp Val Ala Ile Trp Tyr
50 55 60

Asn Ser His Asp Ala Thr Gly Lys Ala Glu Ala Leu Ala Lys Lys Tyr
65 70 75 80

Gly Val Lys Val Lys Ala Tyr Lys Ala Asn Val Ser Ser Ser Asp Ala
85 90 95

Val Lys Gln Thr Ile Glu Gln Gln Ile Lys Asp Phe Gly His Leu Asp
100 105 110

Ile Val Val Ala Asn Ala Gly Ile Pro Trp Thr Lys Gly Ala Tyr Ile
115 120 125

Asp Gln Asp Asp Asp Lys His Phe Asp Gln Val Val Asp Val Asp Leu
130 135 140

Lys Gly Val Gly Tyr Val Ala Lys His Ala Gly Arg His Phe Arg Glu
145 150 155 160

Arg Phe Glu Lys Glu Gly Lys Lys Gly Ala Leu Val Phe Thr Ala Ser
165 170 175

Met Ser Gly His Ile Val Asn Val Pro Gln Phe Gln Ala Thr Tyr Asn
180 185 190

Ala Ala Lys Ala Gly Val Arg His Phe Ala Lys Ser Leu Ala Val Glu
195 200 205

Phe Ala Pro Phe Ala Arg Val Asn Ser Val Ser Pro Gly Tyr Ile Asn
210 215 220

Thr Glu Ile Ser Asp Phe Val Pro Gln Glu Thr Gln Asn Lys Trp Trp
225 230 235 240

Ser Leu Val Pro Leu Gly Arg Gly Gly Glu Thr Ala Glu Leu Val Gly
245 250 255

Ala Tyr Leu Phe Leu Ala Ser Asp Ala Gly Ser Tyr Ala Thr Gly Thr
260 265 270

Asp Ile Ile Val Asp Gly Gly Tyr Thr Leu Pro

<210> 71
 <211> 852
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic gene derived from *Candida magnoliae* NADPH-dependent carbonyl reductase, having numerous codons replaced with others encoding the same amino acids to reduce the free energy of folding

<400> 71
 atggctaata acttctctaa cgttgaatac ccggctccgc cgccagctca caccaaaaac 60
 gaatctctgc aggttctgga cctgttcaaa ctgaacggta aggttgcttc tatcaccggt 120
 tcttctctctg gtatcgggta cgctctgggt gaagcattcg ctccaggtagg tgctgacgtt 180
 gctatctggt acaactctca cgacgctact ggtaaggctg aagctctggc taaaaaatac 240
 ggtgttaaaag ttaaagctta caaggctaac gtttcttctt ctgacgctgt aaaacagacc 300
 atcgaacagc agatcaaaga ctccgggtcac ctggacatcg ttgttgctaa cgctgggtatc 360
 ccgtggacca aagggtgctta catcgaccag gacgacgata aacacttcga tcagggttgtt 420
 gacgttgatc tgaaagggtg ttggttatgtt gctaaacacg ctggccgtca cttccgtgag 480
 cgtttcgaaa aggaaggtaa gaaaggcgct ctggttttca ccgcttctat gtctgggtcac 540
 atcggttaacg taccgcagtt tcaggctacc tacaacgctg ctaaagctgg tgttcgtcac 600
 ttgcgtaaat ctctgggtgt agaattcgct ccgttcgctc gtgttaactc tgtttctccg 660
 ggctacatca acaccgaaat ctctgacttt gtaccgcagg aaactcagaa caaatgggtg 720
 tctctggtac cgctgggccc tggtggcgaa actgctgaac tgggtggtgc ttacctgttt 780
 ctggcttctg acgctgggtc ttacgctacc ggcactgaca tcatcggtga cgggtggttac 840
 accctgccgt aa 852

<210> 72
 <211> 1602
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<400> 72
 atgacagaag ataattattgc tccaatcacc tccgttaaag tagttaccga caagtgcacg 60
 tacaaggaca acgagctgct caccaagtac agctacgaaa atgctgtagt tacgaagaca 120
 gctagtggcc gcttcgatgt aacgccact gttcaagact acgtgttcaa acttgacttg 180

aaaaagccgg aaaaactagg aattatgctc attgggttag gtggcaacaa tggctccact	240
ttagtggcct cggatttggc gaataagcac aatgtggagt ttcaaactaa ggaaggcggt	300
aagcaaccaa actacttcgg ctccatgact caatgttcta ccttgaaact gggatcgcg	360
gcggagggga atgacgttta tgctcctttt aactctctgt tgcccatggg tagcccaaac	420
gactttgtcg tctctgggtg ggacatcaat aacgcagatc tatacgaagc tatgcagaga	480
agtcaagttc tcgaatatga tctgcaacaa cgcttgaagg cgaagatgtc cttggtgaag	540
cctcttcctt ccatttacta ccttgatttc attgcagcta atcaagatga gagagccaat	600
aactgcatca atttggatga aaaaggcaac gtaaccacga ggggtaagtg gacccatctg	660
caacgcatca gacgcgatat ccagaatttc aaagaagaaa acgcccttga taaagtaatc	720
gttcttttga ctgcaaatac tgagaggtac gtagaagtat ctctgggtgt taatgacacc	780
atggaaaacc tcttgacgtc tattaagaat gaccatgaag agattgctcc ttccacgac	840
tttgacgag catctatctt ggaagggtgc ccctatatta atgggttcacc gcagaatact	900
tttggtcccg gcttgggtca gctggctgag catgagggtg cattcattgc gggagacgat	960
ctcaagtcgg gacaaaccaa gttgaagtct gttctggccc agttcttagt ggatgcagg	1020
attaaaccgg tctccattgc atcctataac catttaggca ataatgacgg ttataactta	1080
tctgctccaa aacaatttag gtctaaggag atttccaaaa gttctgtcat agatgacac	1140
atcgctcta atgatatctt gtacaatgat aaactgggta aaaaagttga ccactgcatt	1200
gtcatcaaat atatgaagcc cgtcggggac tcaaaagtgg caatggacga gtattacagt	1260
gagttgatgt taggtggcca taaccggatt tccattcaca atgtttgcga agattcttta	1320
ctggctacgc ccttgatcat cgatctttta gtcatgactg agttttgtac aagagtgtcc	1380
tataagaagg tggaccaggt taaagaagat gctggcaaat tcgagaactt ttatccagtt	1440
ttaaccttct tgagttactg gttaaaagct ccattaacaa gaccaggatt tcaccogggtg	1500
aatggcttaa acaagcaaag aaccgcctta gaaaatTTTT taagattggt gattggattg	1560
ccttctcaaa acgaactaag attcgaagag agattgttgt aa	1602

<210> 73

<211> 533

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 73

Met Thr Glu Asp Asn Ile Ala Pro Ile Thr Ser Val Lys Val Val Thr

1	5	10	15
Asp Lys Cys Thr Tyr Lys Asp Asn Glu Leu Leu Thr Lys Tyr Ser Tyr	20	25	30
Glu Asn Ala Val Val Thr Lys Thr Ala Ser Gly Arg Phe Asp Val Thr	35	40	45
Pro Thr Val Gln Asp Tyr Val Phe Lys Leu Asp Leu Lys Lys Pro Glu	50	55	60
Lys Leu Gly Ile Met Leu Ile Gly Leu Gly Gly Asn Asn Gly Ser Thr	65	70	75
Leu Val Ala Ser Val Leu Ala Asn Lys His Asn Val Glu Phe Gln Thr	85	90	95
Lys Glu Gly Val Lys Gln Pro Asn Tyr Phe Gly Ser Met Thr Gln Cys	100	105	110
Ser Thr Leu Lys Leu Gly Ile Asp Ala Glu Gly Asn Asp Val Tyr Ala	115	120	125
Pro Phe Asn Ser Leu Leu Pro Met Val Ser Pro Asn Asp Phe Val Val	130	135	140
Ser Gly Trp Asp Ile Asn Asn Ala Asp Leu Tyr Glu Ala Met Gln Arg	145	150	155
Ser Gln Val Leu Glu Tyr Asp Leu Gln Gln Arg Leu Lys Ala Lys Met	165	170	175
Ser Leu Val Lys Pro Leu Pro Ser Ile Tyr Tyr Pro Asp Phe Ile Ala	180	185	190
Ala Asn Gln Asp Glu Arg Ala Asn Asn Cys Ile Asn Leu Asp Glu Lys	195	200	205
Gly Asn Val Thr Thr Arg Gly Lys Trp Thr His Leu Gln Arg Ile Arg	210	215	220
Arg Asp Ile Gln Asn Phe Lys Glu Glu Asn Ala Leu Asp Lys Val Ile	225	230	235
			240

Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Val Glu Val Ser Pro Gly
245 250 255

Val Asn Asp Thr Met Glu Asn Leu Leu Gln Ser Ile Lys Asn Asp His
260 265 270

Glu Glu Ile Ala Pro Ser Thr Ile Phe Ala Ala Ala Ser Ile Leu Glu
275 280 285

Gly Val Pro Tyr Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro Gly
290 295 300

Leu Val Gln Leu Ala Glu His Glu Gly Thr Phe Ile Ala Gly Asp Asp
305 310 315 320

Leu Lys Ser Gly Gln Thr Lys Leu Lys Ser Val Leu Ala Gln Phe Leu
325 330 335

Val Asp Ala Gly Ile Lys Pro Val Ser Ile Ala Ser Tyr Asn His Leu
340 345 350

Gly Asn Asn Asp Gly Tyr Asn Leu Ser Ala Pro Lys Gln Phe Arg Ser
355 360 365

Lys Glu Ile Ser Lys Ser Ser Val Ile Asp Asp Ile Ile Ala Ser Asn
370 375 380

Asp Ile Leu Tyr Asn Asp Lys Leu Gly Lys Lys Val Asp His Cys Ile
385 390 395 400

Val Ile Lys Tyr Met Lys Pro Val Gly Asp Ser Lys Val Ala Met Asp
405 410 415

Glu Tyr Tyr Ser Glu Leu Met Leu Gly Gly His Asn Arg Ile Ser Ile
420 425 430

His Asn Val Cys Glu Asp Ser Leu Leu Ala Thr Pro Leu Ile Ile Asp
435 440 445

Leu Leu Val Met Thr Glu Phe Cys Thr Arg Val Ser Tyr Lys Lys Val
450 455 460

Asp Pro Val Lys Glu Asp Ala Gly Lys Phe Glu Asn Phe Tyr Pro Val
 465 470 475 480

Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro Gly
 485 490 495

Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu Asn
 500 505 510

Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg Phe
 515 520 525

Glu Glu Arg Leu Leu
 530

<210> 74
 <211> 1605
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic gene derived from *Saccharomyces cerevisiae* myo-inositol
 -1-phosphate synthase, having numerous codons replaced with other
 s encoding the same amino acids to reduce free energy of folding,
 and a gly codon inserted after the initiating met codon

<400> 74
 atgggtaccg aagataacat cgctccaatc acttctgtta aagttgtaac tgacaaatgt 60
 acttacaaag acaacgaact gctgactaaa tactcttacg aaaacgctgt agtaactaaa 120
 actgcttctg gtcgtttcga tgttactccg actgttcagg actacgtatt caaactggat 180
 ctgaagaaac cggaaaagct gggtatcatg ctgatcggcc tgggtggtaa caacggctct 240
 actctggttg catctgttct ggcaaacaaa cacaacgtag aattccagac taaggaaggt 300
 gttaaacagc cgaactactt tggttctatg actcagtgtt ctactctgaa gctgggcatt 360
 gatgctgaag gtaacgacgt ttacgctccg ttcaactctc tgctgccgat ggtatctccg 420
 aacgacttcg ttgtttctgg ttgggatatc aacaacgcgg atctgtacga agcaatgcag 480
 cgttctcagg ttctggaata tgatctgcaa cagcgtctga aggctaagat gtctctgggt 540
 aagccactgc cgtccatcta ctaccggat ttatcgcag ctaaccagga cgaacgtgct 600
 aacaactgta tcaacctgga cgaaaaggg aacgttacta cccgtggtaa gtggactcac 660
 ctgcagcgta tccgtcgtga tatccagaac ttcaaagagg aaaacgcact ggacaaagtt 720

atcgtactgt ggactgctaa cactgaacgt tacgtagaag tatccccggg tgtaaaccgat 780
 actatggaaa acctgctgca atctatcaag aacgaccacg aggaaatcgc tccgtccacc 840
 atcttcgctg ctgcatctat cctggaaggc gtaccgtaca tcaacggctc tccgcagaac 900
 actttcgtac cgggtctggt acagctgggt gaacacgaag gtaccttcat cgctgggtgac 960
 gatctgaaat ctggccagac taaactgaaa tctgtactgg cacagtctct gggttgacgt 1020
 ggtatcaaac cggtttctat cgcttcttat aaccacctgg gtaacaacga cggctacaac 1080
 ctgtctgctc cgaaacagtt ccgttctaaa gaaatctcta aatcctctgt aatcgacgac 1140
 atcatcgctt ctaacgacat cctgtacaac gacaaactgg gtaagaaagt agatcactgt 1200
 atcgttatca aatacatgaa accggttggt gattctaaag ttgctatgga cgaatactac 1260
 tctgaactga tgctgggagg tcacaaccgt atctctatcc acaacgtttg tgaagactct 1320
 ctgctggcta ccccgctgat catcgacctg ctggttatga ctgaattctg taccgctgta 1380
 tcttacaaga aagttgaccc gggttaaagaa gatgctggca aattcgaaaa cttctaccog 1440
 gttctgacct tctgtcttta ctggctgaaa gctccgctga ctcgctccagg cttccaccog 1500
 gttaacggtc tgaacaaaca gcgtaccgct ctggaaaact tctgcgtct gctgatcggc 1560
 ctgccgtccc agaacgaact gcgtttcgaa gaacgtctgc tgtaa 1605

<210> 75
 <211> 534
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthetic protein derived from *Saccharomyces cerevisiae* myo-inositol-1-phosphate synthase, having a glycine residue inserted after the initiating methionine

<400> 75

Met Gly Thr Glu Asp Asn Ile Ala Pro Ile Thr Ser Val Lys Val Val
 1 5 10 15

Thr Asp Lys Cys Thr Tyr Lys Asp Asn Glu Leu Leu Thr Lys Tyr Ser
 20 25 30

Tyr Glu Asn Ala Val Val Thr Lys Thr Ala Ser Gly Arg Phe Asp Val
 35 40 45

Thr Pro Thr Val Gln Asp Tyr Val Phe Lys Leu Asp Leu Lys Lys Pro
 50 55 60

Glu Lys Leu Gly Ile Met Leu Ile Gly Leu Gly Gly Asn Asn Gly Ser
65 70 75 80

Thr Leu Val Ala Ser Val Leu Ala Asn Lys His Asn Val Glu Phe Gln
85 90 95

Thr Lys Glu Gly Val Lys Gln Pro Asn Tyr Phe Gly Ser Met Thr Gln
100 105 110

Cys Ser Thr Leu Lys Leu Gly Ile Asp Ala Glu Gly Asn Asp Val Tyr
115 120 125

Ala Pro Phe Asn Ser Leu Leu Pro Met Val Ser Pro Asn Asp Phe Val
130 135 140

Val Ser Gly Trp Asp Ile Asn Asn Ala Asp Leu Tyr Glu Ala Met Gln
145 150 155 160

Arg Ser Gln Val Leu Glu Tyr Asp Leu Gln Gln Arg Leu Lys Ala Lys
165 170 175

Met Ser Leu Val Lys Pro Leu Pro Ser Ile Tyr Tyr Pro Asp Phe Ile
180 185 190

Ala Ala Asn Gln Asp Glu Arg Ala Asn Asn Cys Ile Asn Leu Asp Glu
195 200 205

Lys Gly Asn Val Thr Thr Arg Gly Lys Trp Thr His Leu Gln Arg Ile
210 215 220

Arg Arg Asp Ile Gln Asn Phe Lys Glu Glu Asn Ala Leu Asp Lys Val
225 230 235 240

Ile Val Leu Trp Thr Ala Asn Thr Glu Arg Tyr Val Glu Val Ser Pro
245 250 255

Gly Val Asn Asp Thr Met Glu Asn Leu Leu Gln Ser Ile Lys Asn Asp
260 265 270

His Glu Glu Ile Ala Pro Ser Thr Ile Phe Ala Ala Ala Ser Ile Leu
275 280 285

Glu Gly Val Pro Tyr Ile Asn Gly Ser Pro Gln Asn Thr Phe Val Pro
290 295 300

Gly Leu Val Gln Leu Ala Glu His Glu Gly Thr Phe Ile Ala Gly Asp
305 310 315 320

Asp Leu Lys Ser Gly Gln Thr Lys Leu Lys Ser Val Leu Ala Gln Phe
325 330 335

Leu Val Asp Ala Gly Ile Lys Pro Val Ser Ile Ala Ser Tyr Asn His
340 345 350

Leu Gly Asn Asn Asp Gly Tyr Asn Leu Ser Ala Pro Lys Gln Phe Arg
355 360 365

Ser Lys Glu Ile Ser Lys Ser Ser Val Ile Asp Asp Ile Ile Ala Ser
370 375 380

Asn Asp Ile Leu Tyr Asn Asp Lys Leu Gly Lys Lys Val Asp His Cys
385 390 395 400

Ile Val Ile Lys Tyr Met Lys Pro Val Gly Asp Ser Lys Val Ala Met
405 410 415

Asp Glu Tyr Tyr Ser Glu Leu Met Leu Gly Gly His Asn Arg Ile Ser
420 425 430

Ile His Asn Val Cys Glu Asp Ser Leu Leu Ala Thr Pro Leu Ile Ile
435 440 445

Asp Leu Leu Val Met Thr Glu Phe Cys Thr Arg Val Ser Tyr Lys Lys
450 455 460

Val Asp Pro Val Lys Glu Asp Ala Gly Lys Phe Glu Asn Phe Tyr Pro
465 470 475 480

Val Leu Thr Phe Leu Ser Tyr Trp Leu Lys Ala Pro Leu Thr Arg Pro
485 490 495

Gly Phe His Pro Val Asn Gly Leu Asn Lys Gln Arg Thr Ala Leu Glu
500 505 510

Asn Phe Leu Arg Leu Leu Ile Gly Leu Pro Ser Gln Asn Glu Leu Arg
515 520 525

Phe Glu Glu Arg Leu Leu
530

<210> 76
<211> 2043
<212> DNA
<213> Hypomyces rosellus

<400> 76
atgaaacacc ttttaacact cgctctttgc ttcagcagca tcaatgctgt tgctgtcacc 60
gtccctcaca aggccgtagg aactggaatt cctgaaggga gtcttcagtt cctgagcctt 120
cgagcctcag cacctatcgg aagcgccatt tctcgcaaca actggggcgt cacttgcgac 180
agtgcacagt cgggaaatga atgcaacaag gccattgatg gcaacaagga taccttttgg 240
cacacattct atggcgccaa cggggatcca aagccccctc acacatacac gattgacatg 300
aagacaactc agaacgtcaa cggtctgtct atgctgcctc gacaggatgg taaccaaacc 360
ggctggatcg gtcgccatga ggtttatcta agctcagatg gcacaaactg gggcagccct 420
gttgcgctcag gtagttggtt cgccgactct actacaaaat actccaactt tgaaactcgc 480
cctgctcgct atgttcgtct tgctgctatc actgaagcga atggccagcc ttggactagc 540
attgcagaga tcaacgtctt ccaagctagt tcttacacag cccccagcc tggctcttga 600
cgctgggggc cgactattga cttaccgatt gttcctgcgg ctgcagcaat tgaaccgaca 660
tcgggacgag tccttatgtg gtcttcatat cgcaatgatg catttgagg atcccttgg 720
ggatatcact tgacgtcttc ctgggatcca tccactggtt ttgtttccga ccgcactgtg 780
acagtcacca agcatgatat gttctgccct ggtatctcca tggatggtaa cggtcagatc 840
gtagtcacag gtggcaacga tgccaagaag accagtttgt atgattcatc tagcgatagc 900
tggatcccgg gacctgacat gcaagtggct cgtgggtatc agtcatcagc taccatgtca 960
gacggtcgtg tttttacat tggaggctcc tggagcggtg gcgtatttga gaagaatggc 1020
gaagtctata gcccatcttc aaagacatgg acgtccctac ccaatgcca ggtcaacca 1080
atgttgacgg ctgacaagca aggattgtac cgttcagaca accacgcgtg gctcttttga 1140
tggaagaagg gttcgggtgtt ccaagcggga cctagcacag ccatgaactg gtactatacc 1200
agtggaagtg gtgatgtgaa gtcagccgga aaacgccagt ctaaccgtgg tgtagccctt 1260
gatgccatgt gcggaaacgc tgtcatgtac gacgcggtta aaggaaagat cctgaccttt 1320

ggcggtcccc cagattatca agactctgac gccacaacca acgcccacat catcacccctc 1380
 ggtgaacccg gaacatctcc caacactgtc tttgctagca atgggttgta ctttgcccga 1440
 acgtttcaca cctctgttgt tcttccagac ggaagcacgt ttattacagg aggccaacga 1500
 cgtggaattc cgttcgagga ttcaaccccg gtattttacac ctgagatcta cgtccctgaa 1560
 caagacactt tctacaagca gaaccccaac tccattgttc gcgtctacca tagcatttcc 1620
 cttttgttac ctgatggcag ggtatttaac ggtgggtggtg gtctttgtgg cgattgtacc 1680
 acgaatcatt tcgacgcgca aatctttacg ccaaactatc ttacaatag caacggcaat 1740
 ctgcgcacac gtcccaagat taccagaacc tctacacaga gcgtcaaggc cgggtggcaga 1800
 attacaatct cgacggattc ttcgattagc aaggcgtcgt tgattcgcta tggtagacgcg 1860
 acacacacgg ttaatactga ccagcgcgcg attccctga ctctgacaaa caatggagga 1920
 aatagctatt ctttccaagt tcttagcgac tctggtgttg ctttgctgg ctactggatg 1980
 ttgttcgtga tgaactcggc cgggtgttct agtgtggctt cgacgattcg cgttactcag 2040
 tga 2043

<210> 77
 <211> 680
 <212> PRT
 <213> *Hypomyces rosellus*

<400> 77

Met Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
 1 5 10 15

Val Ala Val Thr Val Pro His Lys Ala Val Gly Thr Gly Ile Pro Glu
 20 25 30

Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
 35 40 45

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
 50 55 60

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp
 65 70 75 80

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
 85 90 95

Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
100 105 110

Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val
115 120 125

Tyr Leu Ser Ser Asp Gly Thr Asn Trp Gly Ser Pro Val Ala Ser Gly
130 135 140

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr
180 185 190

Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu
195 200 205

Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val
210 215 220

Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val Ser
245 250 255

Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
275 280 285

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
290 295 300

Pro Asp Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Met Ser
305 310 315 320

Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val Phe
325 330 335

Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly
355 360 365

Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly
370 375 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385 390 395 400

Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
405 410 415

Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
420 425 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp
435 440 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly
450 455 460

Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg
465 470 475 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr
485 490 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe
500 505 510

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn
515 520 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
530 535 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
 545 550 555 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn
 565 570 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr
 580 585 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser
 595 600 605

Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val
 610 615 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly
 625 630 635 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro
 645 650 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val
 660 665 670

Ala Ser Thr Ile Arg Val Thr Gln
 675 680

<210> 78
 <211> 2046
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic gene derived from Hypomyces rosellus galactose oxidase,
 having numerous codons replaced with others encoding the same am
 ino acids to reduce free energy of folding and a gly codon insert
 ed after the initiating met codon to insert a restriction site

<400> 78
 atgggcaagc atctgctgac tctggcactg tgtttctctt ctatcaacgc tgttgctgta 60
 accgttccgc ataaggctgt tggtagcggg atcccgggaag gttctctgca gttcctgtct 120
 ctgcgtgctt ctgctccgat cggttctgct atctctcgta acaactgggc agttacctgc 180
 gactccgcac agtctggtaa cgaatgcaac aaagctatcg acggtaacaa agacactttt 240
 tggcacactt tctatggcgc taacggcgac ccgaaaccgc cgcacaccta caccatcgat 300

atgaaaacca	ctcagaacgt	aaacggcctg	tctatgctgc	cgcgccagga	tggttaaccag	360
aacggttgga	ttggtcgtca	tgaggatatat	ctgtcttccg	atggtactaa	ctgggggttct	420
ccggtagctt	ctggctcctg	gttcgctgac	tctaccacca	aatactctaa	cttcgagact	480
cgtccggcac	gctatgtacg	cctggttgct	attactgagg	caaacgggtca	gccgtggacc	540
tctatcgcag	aaattaacgt	tttccaggca	tcttcttaca	ccgctccgca	gccgggtctg	600
ggtcgctggg	gtccgactat	tgacctgccg	atcgttccgg	cagctgctgc	tattgagccg	660
acttctggtc	gtgttctgat	gtggctcttct	taccgtaacg	acgctttcgg	tggttctccg	720
ggcggcatca	ccctgacctc	ttcttgggat	ccgtctactg	gcatcgtttc	cgatcgtaacc	780
gtaactgtta	ctaagcacga	tatgttttgt	ccgggtattt	ctatggatgg	caacggccag	840
attgtagtaa	ctggtggcaa	cgacgctaaa	aaaacctctc	tgtatgattc	ctcctctgat	900
tcttgatcc	cggttccgga	catgcaggta	gctcgcgggt	atcagtcttc	cgctactatg	960
tctgatggcc	gtgttttcac	tattggtggt	tcttggtctg	gcggcgattt	tgagaaaaac	1020
gggtgaagttt	actctccatc	ctccaaaact	tggacttccc	tgccgaacgc	taaagttaac	1080
ccgatgctga	ctgcagataa	gcagggcctg	taccgttccg	ataaccacgc	atggctgttt	1140
ggctggaaaa	aaggctccgt	atttcaggct	ggtccgtcta	ctgctatgaa	ctggtactat	1200
acttctgggt	ctggcgatgt	taagtccgct	ggcaagcgtc	agtctaaccg	tggcgtagca	1260
ccggatgcta	tgtgcggtaa	cgctgttatg	tacgatgctg	taaagggcaa	gattctgact	1320
tttggtggt	ctccggacta	tcaggactcc	gacgtacta	ctaacgcaca	tatcattact	1380
ctgggtgagc	cgggtacctc	tccgaacact	gtatttgcat	ctaacggcct	gtactttgct	1440
cgtacctttc	acacctctgt	agtactgccg	gatggttcca	cttttatcac	tggcggtcag	1500
cgcgcgggta	ttccgttcga	ggactctact	ccgggtttca	ccccggagat	ctacgtaccg	1560
gagcaggata	ctttctacaa	gcagaaccgc	aactccattg	ttcgtgtata	ccactctatc	1620
tctctgctgc	tgccggatgg	tcgtgtattt	aacggtggtg	gtggtctgtg	tggcgactgt	1680
actactaacc	atttcgatgc	gcagattttt	accccgaaact	atctgtataa	ctctaacggt	1740
aacctggcaa	ctcgcccgaa	aattactcgc	acttctaccc	agtctgtaaa	ggtaggcggc	1800
cgtatcacca	tctctaccga	ctcttctatc	tctaaagctt	ctctgattcg	ctatggtaacc	1860
gctacccata	ctgtaaacac	tgaccagcgt	cgtatcccgc	tgacctgac	caacaacggt	1920
ggtaactctt	actcttttca	ggttccgtct	gactctggtg	ttgctctgcc	gggttactgg	1980

atgctgttcg ttatgaactc tgctggtggt ccgctctgttg cttctaccat ccggtgttacc 2040

cagtag 2046

<210> 79

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic protein derived from Hypomyces rosellus galactose oxidase, having a glycine residue inserted after the initiating methionine

<400> 79

Met Gly Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn
1 5 10 15

Ala Val Ala Val Thr Val Pro His Lys Ala Val Gly Thr Gly Ile Pro
20 25 30

Glu Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly
35 40 45

Ser Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln
50 55 60

Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe
65 70 75 80

Trp His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr
85 90 95

Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met
100 105 110

Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu
115 120 125

Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp Gly Ser Pro Val Ala Ser
130 135 140

Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr
145 150 155 160

Arg Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly
165 170 175

Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser
180 185 190

Tyr Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp
195 200 205

Leu Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg
210 215 220

Val Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro
225 230 235 240

Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val
245 250 255

Ser Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly
260 265 270

Ile Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp
275 280 285

Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro
290 295 300

Gly Pro Asp Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Met
305 310 315 320

Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val
325 330 335

Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr
340 345 350

Ser Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln
355 360 365

Gly Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys
370 375 380

Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr

385		390		395		400
Thr Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn						
	405		410		415	
Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp						
	420		425		430	
Ala Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln						
	435		440		445	
Asp Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro						
	450		455		460	
Gly Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala						
	465		470		475	480
Arg Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile						
	485		490		495	
Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val						
	500		505		510	
Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln						
	515		520		525	
Asn Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu						
	530		535		540	
Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys						
	545		550		555	560
Thr Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr						
	565		570		575	
Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser						
	580		585		590	
Thr Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser						
	595		600		605	
Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr						
	610		615		620	

Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly
625 630 635 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu
645 650 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
660 665 670

Val Ala Ser Thr Ile Arg Val Thr Gln
675 680